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November 16, 2004, 20:27:58; Search time 16892 Seconds (without alignments) 11573.266 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		% Onerv				
No.	Score	Match	Match Length DB	DB	ΩI	Description
-1	4134	100.0	4134	9	AR182343	AR182343 Sequence
8	4134	100.0	4134	9	AR236221	AR236221 Sequence
٣	4134	100.0	4134	9	AR243543	AR243543 Sequence
4	4134	100.0	4134	9	AR254415	AR254415 Sequence
Ŋ	4134	100.0	4134	9	AR321738	AR321738 Sequence
ω	4134	100.0	4134	9	AR411424	AR411424 Sequence
7	4134	100.0	4134	9	AR432994	AR432994 Sequence
α	4134	100.0	4134	9	AX417770	AX417770 Sequence
σv	4134	100.0	4134	9	AX449101 ·	AX449101 Sequence
10	4134	100.0	4134	9	AX743965	AX743965 Sequence
11	4116	99.66	4116	ស	AF406649 .	AF406649 Squalus a
12	1745.2	42.2	3234	9	BD205377	BD205377 G protein
13	1745.2	42.2	3234	9	AX542191	AX542191 Sequence
14	1745.2	42.2	3783	9	CQ714283	CQ714283 Sequence
1.5	1745.2	42.2	3783	9	AX548832	AX548832 Sequence
16	1745.2	42.2	3783	σ	HSU20759	U20759 Human parat
17	1745.2	42.2	3809	9	AR012624	AR012624 Sequence
18	1745.2	42.2	3809	ø	AR028467	AR028467 Sequence
19	1745.2	42.2	3809	Ø	AR078219	AR078219 Sequence

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AR145170 Sequence AR177783 Sequence 175053 Sequence AX429806 Sequence AX702238 Sequence BX240871 Sequence BX24086 Sequence SR176 Homa Sapien S83176 Homa Sapien D50855 Human mRNA S67307 Ca(2+)-sens AR012622 Sequence AR078217 Sequence AR078217 Sequence AR078217 Sequence AR078218 Sequence AR078286 Sequence AR17782 Sequence	ALIGNMENTS 4134 bp DNA linear PAT 20-APR-2002 S 6337391. S.E.M. and Hebert, S.C. tor in aquatic species and methods of use lers lers own"	DNA" 34; DB 6; Length 4134; 0; ches 0; Indels 0; Gaps 0;	AATTCCGTTGCTGCTCGGTTCAGTCCTCCTCCAGTGCAAATGAGAAATGGGGGGTC 60 AATTCCGTTGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAAATGGTGGTC 60 AATTCCGTTGCTGTCGCTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAAATGGAAATGGTGGTC 60 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 GCCATTACAGGAACATGCACTACTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120
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SM Unknown.

Unclassified.

CE 1 (bases 1 to 4134)

NS Harris, Hw. Jr., Russell, D.R., Nearing, J. and Bet's Harris, Hw. Jr., Russell, D.R., Nearing, J. and Bet's Harris, Hw. Jr., Russell, D.R., Nearing, J. and Bet's Harris, Hw. Jr., Russell, D.R., Nearing, J. and Bet's Harris, Harris, Hw. Jr., Russell, D.R., Nearing, J. and Bet's Harris, Indels . 9 . 0 DB Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 4134 bp patent US 6463883. GI:27280030 from AR236221 Sequence 17 f AR236221 AR236221.1 3601 3601 3661 3661 3721 3721 3781 3781 3841 3841 3901 3901 3961 3961 4021 4021 4081 4081 121 RESULT 2
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SOURCE ORGANISM Unknown. ORGANISM Unknown. Unclassified. Inclassified. AUTHORS Harris, H. W. Jr., Russell, D.R., Nearing, J. and Betka, M. TITLE Methods for raising pre-adult anadromous fish OUGNAL Patent: US 654747-A 17 20-MAY-2003; FRAUTES Location/Qualifiers Source /organism="unknown" /mol_type="genomic DNA"	Leng Inde AAA! AAA! TIG	Db 61 GCCATTACAGGAACATGCACTACTCTGTAATGAAATATTGTCAGAAGT 120 OY 121 TATTAAATGTTTCTGCAAGGATGGCTTCACGAAAATCTGCAAGTTTTCCCATT 180	Db 181 GTCATTGTATGATAACTGACCAAAGGGATGTAACAAATGGAACAAAGGTGAGGACCAC 240 OY 241 GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAACATGAGGAGAA 300 Db 241 GTTCACCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAAGACTTGAGGAGAA 300 OY 301 ATGGGGATTGATCTTCGAGGAGTTCTTGCAGGAGTTCTTGAGAAGATAA 360	Db 301 AIGGGGATTGATCTTCCAGGAGTTCTGCTGAAAGCGATCCCTCACCATTACAAAATAA 360 Qy 361 GCAGAAATCCTCCAGGCATCCTCTGAAACGGCTGGCGTAGTGAGTTAGGAA 420 Db 361 GCAGAAATCCTCCAGGCATCGTTAAACGGCTGGCGTAGTGGTTGAGTCAAGGAA 420 Qy 421 CAGAAAATCCTCCAGGTTCAACTGCCAACTCTTATTCTTGGGATTAA 480	Db 421 CAGAGACTGCACATGGTTCACTGCCACTCTTATTCTTGGGATTTACA 480 Qy 481 CTCCTACAGTGCTACAATGTCTCAGGGTATGGTCCAAAGGGCCCAGAAAAAGA 540 Db 481 CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAAGGGCCCAGAAAAGA 540 Qy 541 GACATCATAGTGGGGAGTCTTCCCAATACACTTTGGAGTAGCGCCCAGAAGGATCAGGAC	541 GACATCTGGGAGGTCTTTTCCCATACACTTGGAGTGCCGCCAGGGTC 601 TTAAAATCGAGACCGGAGACACAAAGATTTCGGGCTTC 601 TTAAAATCGAGACCGGAGACACAAAATGTATTCGGTACAATTTCGAGGCTTC 601 TTAAAATCGAGACCGAGGCACAAAATGTATTCGGTACAATTTTCGAGGCTTC	

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QY 3841 TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT 3900 (\$ g	361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
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LOCUS AX449101 4134 bp DNA Innear PAT 03-JUL-2002 DEFINITION Sequence 23 from Patent WO0230215. ACCESSION AX449101 VERSION AX449101.1 GI:21697918	ço, do	721 ATCACCCTGGGATATCGCATATTTGACACGTGTAACACCGTGTCCAAGGCGCTAGAGGCA 780
ORGANISM Mustelus canis (smooth dogfish) ORGANISM Mustelus canis Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	yo da	781 ACACTCAGCTTTGTGGCCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 840
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source 1.4134 /organism="Mustelus canis" /mol_type="unassigned DNA" /db_xref="taxon:7812"	yo da	961 AGCAGGCTCCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT 1020
Oktoin Query Match Best Local Similarity 100.0%; Score 4134; DB 6; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; Matches 4134; Concernative 0. Maccarde 0. 174615 0. Gang 0.	VQ da	1021 GAGCAACAGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGG
1334, CONSELECTIVE 0; MINNACCHES 0; INGELS 0; CAPS 1 AATHCCGTTGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAAATGGTGGTC 60 1 AATHCCGTTGCTGTCGTTCAGTCCAAGTCTTCTTCTAGTGAAAAATGAGAAAATGAGTGTC 60	Qy	1081 ACCCTGGCGGCGACGATGACTATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGAGGGCC 1140
61 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATTGTCAAGGT [λ ₀ α ₀	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGACATGATCTCTCAGTACTACACCCGGAAG 1200
121 TATTAAAATGTTTCTGCAAGATGGCTTCAGGAAATCAATC	. ठे वि -	1201 CAGITGGAGITCATCGCCGACGTCATCCAGAACTCCTCGGCCAAGGTCATCGTGGTCTTC 1260
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1312 CORNECTOR CONCOUNTED AND ADDRESS OF THE PROPERTY OF T	2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACC 2400	1 AACCGGGAGTIGICCTACCTGCTGTTCTCCCTCATCTGCTGCTTCTCCGGCTCGCTC	2461 AICHTCAICGGCGAGCCCAGGACTGGACCTGTCGGCTCCGCCAACGGCCTTTGGCAIC 2520	2521 AGCTTCGTCCTGTGCATCCTGGTGAAGACCAACCGGGTGCTGCTGCTGCTTC 2580 2521 AGCTTCGTCCTGTGCATCCTGGTGAAGACCAACCGGGTGCTGCTGGTGAAGACCAACCGGGTGCTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCGGGTGCTGGTGAAGACCAACCA	581 GAGGCCAAGATCCCCACCAGCCTCCACCACAGTGGGTGGCCTCAACCTGCAGTTCCTC 264	cresterrectroscarcenergenaricereactisearcareactises 2707	701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCATCATCATCACCTGCGAC 278	761 GAGGGCTCGTTCGTGGCGCTGGGCTTCCTCATCGGCTACCTGCCTCTCGCCCCTC 282 [11	821 IGCTICTICTICGCCTICAAGTCCCGTAAGCTGCCGAAAACTTCAACGAGGCTAACTT	294		6 % 8 %	061 AAAACCATCGAGAAGGTGCGCTGCAGCACGCGCCCACCCTCAAGGTGGCGCCCGG	GCCACCCTCCGGCGCGCCGCGCGCTCTCGCAAGCGCTCCAGCAGCCTGGCGGCTCCACCAGCTGTGCGCGCGC	181 ATCTCCTCGCCCCCTCGTCCACGGGGCGGGCCTCACCATGGAGATGCAGGCTCGC 3	3241 AGCACGCAGAAGGTCAGCTTCGGCACCGCACCGTCACCCTGTCGTTCGACTTCGAGGAG 3300	ACAGGCCGATACGCCACCCTCAGCCGCACGCAGCAGAAACTCGGCGGATGGCCGC 336	342	3421 CAGCCGCCAACGATGCCGATACAAGGCGGCGCCCAACCAA
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		1261 TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGAT 132. 1321 CGGATCTGGCTGGCCGAGCGTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAAGGAATC 138.	1321 CGGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATGCCAAGCCAGAGTAC 138 1381 TTCCACGTGGTCGGCGGCACCATCGCTTCGCTCTCAGGGGGGGG	1441 PACAAGTTCCTGAAGGAGGTCCAGCAGGTCCTCGAACAAGAGGTTTGTCAAGGAG 150 1441 PACAAGTTCCTGAAGGAGGTCCACCAGGAGTCCTCGAACAATGAGTTTGTCAAGGAG 150 1441 PACAAGTTCCTGAAGAGGTCCTCAAGAGATCTTGAACAATAAGGTTTTGTCAAAGAG 150	1501 TTCTGGGAGGACTTCAACTGCTACTTCACCGAGAAGACCTGAGGCAGCTGAAGAAT 156 1501 TTCTGGGAGGACTTCAACTGCTACTTCACCGAGAAGACCTGACGCAGCAAGAAA 156	1561 TCCAAGGTGCCCTGGCACCGGCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC 162 1561 TCCAAGGTGCCCTCGCACCGACCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC 162	1621 AGACGGACAGCCCTACGCCACCCCTGGAGGAGGAACATCACCAGCGTGGAGACC 168 1621 AGACGGACACCCTACGCCACCCTGCACTGGGAGGAACATCACCAGCGTGGAGAACC 168	1681 CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC 174	1741 ATTGCTCACGCCTGCAAGACATCCACTCTTGCAAACCCGGCACGGGCATCTTTGCAAAC 180	1801 GGATCTTGTGCAGATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGTGT 186	1861 CTGAAGTTTACCAACAGCATGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 192	1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCAT 198	1981 GAGGTGGGCAACTACAACGCCTACGCTAAGCCCAGTGACCGACTCAACGAAGAAAG 204 1981 GAGGTGGGCAACTACAACGCCTACGCTAAGCCCAGTGACCGACTCAACATCAACGAAAAA 204	2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCGAGACTGT	2101 GTGCCGGCACCAGGAAGGGAATCATCGAGGGGAGGCCACCTGCTGCTTTGAATGCATG	2161 GCATGTGCAGAGGGAGAGTTCAGTGAAAAACGATGCAAGTGCAGTGTACAAAGTGCCG 2	2221 AATGATTTCTGGTCGAATGAGAACCACGTCGTGCTTCGTCCAGGAGATCGAGTACTG 228 2221 AATGATTTCTGGTCGAATGAGAACCACACGTGGTTCGTGCTTGGTGATTGTTGTTACTG 228 2221 AATGATTTCTGGTCGAATGAACCACACACGTGGTTGCTTGC	2281 TCGTGGACGGAGCCCTTCGGGATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATC 23	2341 ACCICCITCGTGGGGGTCTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACC

Qy 3481 GGGGGGAGGAGGGGCCCCACACTATGGAAGGAAACCTAATCCAACTCCTCCTCATCAAC 3540	Matches 4134; Conservative 0; Mismat	,
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99 3601 TGCCGAACCTCTCCGCCACTTCGGTTTTGCTGAAGATTGCAGCATCTGCAGT 3660	121	
Qy 3661 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAAC 3720	181 .	
OY 3721 ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAACTTATCTGAACT 3780	2 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30
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QY 3901 CACTGACATTGCCACTGTGATCACAACTGTTTATAACATTTATCATTGAAACTGGA 3960 	4212 C	6 6
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OY 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	601	
AX743965 4134 bp	QY 661 CTCCAGGCAATGATATTCGCAATTGAAGAGATTAACAACAGGATTTGACTTTCC	AGTATGACTTTCCTGCCCAAT 720
Sequence 7 from Patent AX743965 AX743965.1 GI:3072265	2) ATCACCCTGGGATATCGCATATTTGACACGTGTACACCGTGTCCAAGGCGG	3TGTCCAAGGCGCTAGAGGCA 780
SOURCE Squalus acanthias (spiny dogfish) ORGANISM Squalus acanthias Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Squaliformes; Squaloidei;	781 ACACTCAGCTTTGTGGCCCAGAACAAATC	TTCTGTAAC TTCTGTAAC
Squalidae; Squalus. CE 1 RS Harris,J.H., Jury,S., Russel,D.R., Nearing,J., Be and Brown,E.M.	OY 841 IGCTCTGACCATACCACAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC	GCAACCGGGTCAGGAATCTCC 900
E NAL ES	QY 901 ACGGCTGTGGCCAATCTATTGGGATTATTTTACATTCCACAGGTCAGCTATGCCTCCTCG	DAGGICAGCIAIGCCICCCCC 960
<pre>source 14134 /organism="Squalus acanthias" /mol_type="genomic DNA" /db_xref="taxon:7797"</pre>	Qy 961 AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCAAAGAATGAGTGACAAGGCTTCCTGAGGACCATCCCCAATGATGAGATGAGATACAAGGCTTCCTGAGGACCATCCCCAATGATGAGATACAAGGCTTCCTGAGGACCATCCCCAATGAT	TGAGGACCATCCCAATGAT 1020
ORIGIN Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0;	OY 1021 GAGCAACAGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGAACTGGGTGGG	TTCCAGTGGAACTGGGTGGA 1080
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Squalus acanthias (spiny dogfish)
Squalus acanthias
Squalus acanthias
Usukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Squaliformes, Squaloidei,
Squalidae, Squalus.

4116 bp mRNA linear VRT 21-MAR-2003 Squalus acanthias calcium polyvalent cation receptor/salinity sensing protein mRNA, complete cds.

DEFINITION

RESULT 11 AF406649 LOCUS AF406649.1 GI:21842084

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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ISSPASSTCGPGLIMEMQRCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSAD
GRSGDDLPSRHHDQGPPQKCEPQPANDARYKAAPTKGTLESFGGSKERPTIMEET"
l (bases 1 to 4116)
Nearing, J., Betka, M., Quinn, S., Hentschel, H., Elger, M., Baum, M.,
Bal, M., Chattopadyhay, N., Brown, E.M., Hebert, S.C. and Harris, H.W.
Polyvalent cation receptor proteins (Caks) are salinity sensors in fish
proc. Natl. Acad. Sci. U.S.A. 99 (14), 9231-9236 (2002)
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Nearing, J. and Harris, W.
Direct Submission
Submitted (0.5 AUG-2001) MariCal, 400 Commercial Street, Portland,
ME 04101, USA
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/db_xref="taxon:7797"
/tissue type="kidney"
439, .3522
/note="G protein-coupled receptor"
/codon start=1
/product="calcium polyvalent cation receptor/salinity
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    .4116
    /organism="Squalus acanthias"

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/db_xref="G1:21842085"
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Db 3661 TGCCCAACCTCCCCCTCTCGGCACTTTGCGTTTTGCTGAAGATTGCAGGT 3660 Qy 3661 TCCTTTATCCCTGATTTCTGACTTGGGTTTTACTGGATGGA	RESULT 12 BD205377 BD20531480-A/1 BD205377 BD20531480-A/1 BD205374 BD205374 BD20531480-A/1 BD205374 BD20531480-A/1 BD205314
	3061 AACACCATCGAGGAGGTGCAGCACGCGGCCCACGCCTTCAAGGTGGGGCCCGG 3120

Oy 1521 CTGCTACTCACCGAGAAGACCCTGACGACGAGATTCCAAGGTGCCCTCGCACGG 1580 Db 1071 CTGCCACCTCCAAGAAGGTGCAAAAGGACCTTTACCTGTGGACACTTTCTG 1122 Qy 1581 ACCGGCGGCTCAAGGGAGACGCGGGGAACTCCAGACGACACCCTACGCC 1640 Db 1123 AGAGTCACGAGAAAAGGCGGGGAACTCCAGACGCCTACGACACCTTCCGACC 1178 Qy 1641 CCCCTGCACTGGGGAAGAACATCACCAGCGTGGAGAACCCCTACCTGGATTATACACA 1700 Db 1164	QY 1701 CCTGAGGATCTCCTACAATGTATGTGGCCGTCTACTCCATTGCTCAGCCCTGCAAGA 1760 Db 1239 TTTACGGATATCCTACAATGTGTACTTAGCAGTCTACTCCATTGCCACGCCTTGCAAGA 1298 QY 1761 CATCCACTCTTGCAAACCCGGCACGGCATCTTTGCAAACGGATCTTAA 1820 Db 1299 TATATATACTGGGAAGAGGCTCTTCACCAATGCTGTGCAGACATCAA 1358	Oy 1821 AAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCAGCATTACCAACAGCAT 1880	Oy 1941 CTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGCTTCCATGAGGTGGGCAACTACAACGC 2000 1479 CTGGCACCTCTCCCCAGAGGATGGCTCCATGGTGTTTAAGGAAGTCGGGTATTACAACGT 1538 QY 2001 CTACGCTAAGCCCAGTGACCTCAACAACAACAAAATCCTCTGGAGTGGCTT 2060 Db 1539 CTATGCCAAAAAAGAAAAAAAAAACTCTCTCTACCAACAAAAAATCCTGTGGAGTTGGTT 1598	2061 CTCCAAAGTGGTTCCTTTCTCCAACTGCAGACTGTGGCGGGGCACCAGGAAGGG 212	OY 2181 CAGTGATGAAAACGATGCGAGTGTACAAAGTGCCGAAATGATTTCTGGTCGAATGA 2240 DD 1719 TAGTGATGAGACAGTGCCTGTAACAAGTGCCCAGATGATTTCTGGTCCAATGA 1778 QY 2241 GAACCACACGTGGTGCATGCCTGTAAGATACCTGTCGTGGAGAGCCCTTCGG 2300 DA 1770 GAACCACACGTGGTGCATGGCAAGGAGATCGAGTACCTGTGGAGAGCCCTTCGG 2300 DA 1770 GAACCACACGTGGTGCATGGCAAGGAGATCGAGTACCTGTGGAGAGCCCTTTCGG 1838	2301 GATGCTCTGACCATCTTGGCGTACTGGGGCATCCTGATCACCTCCTTGTGGGGGT 1839 GATGCTCTCACCCTCTTTGCGGGCATTTTCCTGACGCTTTTGTGTGTG	2421 GCTGCTCTCCCTCATCTGCTGCTTCTCCAGCTCGTCATCTTCATCGGCGAGCCCAG 1959 CTCCTCTTCTCCCTGCTGCTGCTTCTCCAGCTCCTTTCTTCATCGGCGAGCCCCAG 2481 GGACTGGACCTGTCGGCCCCAACCGGCCTTTGGCATCGTCTTGTGTGTG	2541 CTGCATCCTGGTGAAGACCAACCGGGTGCTGGTTCTTCGAGGCCAAGATCCCCACCAGGTGTTCTTCGAGGCCAAGATCCCCACCAGGTGTTTCTGAGGCCAAGATCCCCACCAGGTGTTCTTCTGAGGCCAAGATCCCCACCAGGTGTTCTTCTGAGGCCAAGATCCCCACCAGGTGTTCTCTCTC
Query Match 42.2%; Score 1745.2; DB 6; Length 3234; Best Local Similarity 76.4%; Pred. No. 7.6e-273; Indels 17; Gaps 3; Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3; 501 CTCAGGGTATGGTCCAAACCAAACAAGAACAAAAAAAAAA	GACAAATGITCATITGGATACAATTTTCGAGGCTTCCGATGGCTCCAGGCCGGAGGTCGGGCGAAAATGTTCGGTACAAAATGTATTCGGTACAAGGCTTCCGATGGCTCCAGGCGATGATATTCGCTTCGGTGTCGCTTCGGCGTATACAGGTATATTCCGTGGGTTTCGCTTCCGCGCGGGTATAACAACAATATCCTGCCCAATATCACCCTGGGATATCGCATATCGCATATCACCTTGGAGTATACGCATATCACCTTGCATATCACCCTGGGGATATCGCATATCACCTTGCATATCACCCTGGGATATCGCATATCACCTTACACCTTGCATATCACCTTACACCTTACACCTTACACCTTACACCTTACACCTTACACACTTACACCTTACACCTTACACCTTACACCTTACACACTTACACCTTACACACACATATCACCTTACACACACATATCACCTTAC		CACAATAGCAGTGGGGGCAACGGGTCAGGAATCTCCACGGTGTGGCCAATCTATT 92 TACGATTGCTGGGGGCAACGGGTCAGGGTGTGCCAGGCGATGTGT 92 TACGATTGCTGGGGGGAGTGGGGGCTCAGGGGATGGCAATGTGT 47 GGGATTATTTACAATTCCACGGGTCAGGCTCTCCTCGAGCAGGAATGCCT GGGATTATTTACACACGGCAGGTCAGCTATGCCTCCTCGAGCAGGAACGCAACGGAAA 98	GGGGCTCTTCTACATTCCCCAGGTCAGTTATGCCTCCTCCAGCAGACTCCTCAGCAACAA GAATGAGTACAAGGCCTTCCTGAGGACCATCCCCCAATGATGAGCAACAACAA [711 CGACTTCAGTGAACTCATTCCCAGTACTCATGAGGAATCCAGCATGTGGTAGA 770 1221 CGTCATCCAGAACTCCTCGGCCAAGGTCATCTCTCCAATGGCCCCCGACCTGCA 1280	831 GCCCTCATCAAGAATTGTCCGAATATCACGGCAAGATCTGGCTGG	951 CATTGATTCCTCTCAAGGTGGGCAGATCCCAGGCTTCCGGGAATTCCTGAAGAAGCT 1010 1461 CCACCCCAGCAGGTCCTCGGACAATGGGTTTGTCAAGGAGTTCTGGGAGGAGACCTTCAA 1520 1161 CCATCCCAGGAAGTCTGTCCCAAGGAGTTTTGCCAAGGAGTTTTGGGAAGAAACATTTAA 1070 1011 CCATCCCAGGAAGTCTGTCCACAATGGTTTTGCCAAGGAAGTTTTGGGAAGAAACATTTAA 1070

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                                                                                                     17;
                                                              DB 6; Length 3234;
                                                                                                        Indels
                                                            Score 1745.2; DB 6;
Pred. No. 7.6e-273;
0; Mismatches 658;
/db_xref="taxon:9606"
                                                              Query Match
Best Local Similarity 76.4%;
Matches 2187; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Garrett, J.E. and Simin, R.T.
G-protein tusion receptors and chimeric gaba b? receptors Patent: WO 0.299033-A 18 11-APR-2002;
NPS PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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1011 CCATCCCAGGAAGTCTGTCCACAATGGTTTTGCCAAGGAGTTTTGGGAAGAAACATTTAA 1070 1521 CTGCTACTTCACCGAGAAGACCCTGACGACGTTCCAAGGTGCCCTCGCACGG 1580 1521 CTGCTACTTCACCGAGAAGACCTGAAGAATTCCAAGGTGCCCTCGCACGG 1580 1071 CTGCCACTCCAAGAAAGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTG 1122 1581 ACCGGCGGCTCAAGGGGGACGCTCCAAGGCGGAAACTCCAGACGACAGCCCTAAGGCA 1640		1701 CCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACCATGCTCACGCCCTGCAAGA 1760 1239 TTTACGGATATCCTACAATGTGTACTTAGCAGTCTACTCCATTGCCCACGCCTTGCAAGA 1298 1761 CATCCACTTTGCAAACCGGCACTTTGCAAACGGATCTTGTGCAGATATTAA 1820	1299 TATATATACCTGCTTACCTGGGAGGGCTCTTCACCAATGGCTCCTGTGCAGACATCAA 1358 1821 AAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT 1880	1881 GGGTGAGCAGGTTGACGATCAAGGTGACCTCAAGGGGAACTACACCATTATCAA 1940	1479 TIGGCACTTTCCCCAGAGGATGCTCCATCGTTTTAAGGAAGTCGGGTATTACACGT 1538 2001 CTACGCTAAGCCCAGTGACCGACTCACATCGAAAAAAAAA		2121 GATCAICGAGGGGAGCCCACCTGCTTTGAATGCAIGGCATGGCAGAGAGAGTT 2180 	2181 CAGTGATGAAACGATGCAAGTGCGTACAAAGTGCCCGAATGATTTCTGGTCGAATGA 2240		1839 ĠATĊĠCAĊŢĊĠĊĊŢĊŢŢĠĊĠŢĠĊŢĠĠĠĠĀŢŢŢĊĊŢĠĀĊĀĠĊĊŢŢŢĠŢĠĊŢĠĠŢĠŢ 1898 2361 CŢŢĊAŢCAAGTĄĠĠAŖĊĄĊŢĊĊĠŢĊĠŢĠĠĠĠĠĠŢĊŢŢĠĊŢŢĠĊŢŢĠĊŢ CŢŢĊAŢĊAĀĠŢŢĊĀĠĠAŖĊŖĊĊĊŖŢĊĠŢĠŖĠĸĠĠĠĠĠĠĸĠĠŖŢĠŢĊĊŢŖĊĊŢ 2420	2421 GCTGCTCTTCTCCCTCATCTGCTTCTCCAGCTCGCTCATCTTCATCGGCGAGCCCAG 2480	2481 GGACTGGACCTGTCGCCAACCGGCCTTTGGCATCGCTTCGTCCTGTGCATCTC 2540 2019 GGACTGGACCTGCGCCAGCCGGCCTTTGGCATCTGGCTTCGTGCATCTC 2078	2541 CTGCATCCTGGTGAAGACCAACCGGGTGCTGGTCTTCGAGGCCAAGATCCCCACCAG 2600 2079 ATGCATCCTGGTGAAAACCAACCGTGTCTCTGGTGTTTGAGGCCAAGATCCCCACCAG 2138

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Best Local Similarity 76.4%;
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Lifespan Biosciences, Inc. (US)
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PAT 26-NOV-2002 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. linear AX548832 3783 bp DNA Sequence 117 from Patent W002061087. AX548832 AX548832.1 GI:25813725 Chordata; Primates; Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, C Mammalia, Eutheria, P RESULT 15
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Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRB), antibodies thereto, and systems for identifying such antigenic peptides

REFERENCE AUTHORS TITLE

1040 1100 1160 1142 1322 ñ 800 860 920 842 980 962 740 722 782 560 482 620 542 680 602 662 ATTIGACACTIGCAACACGITICIAAGGCCTIGGAAGCCACCCTGAGTTTTGITGCTCA GGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTACTTCCACGTGGTCGGCGGCACCCCTGGGCCAGCCTCCACGTGCTCCACGTGCTTCCACGTGGTTGGCGGCAC GAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGATGAGCAACAGGCCACAT GAATCAATTCAAGTCTTTCCTCCGAACCATCCCCAATGATGAGGACCACAGGCCACTGCCAT GAACAAAATCGACTCGACTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC CACAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCCACGGCTGTGGCCAATCTATT GGGAITATTTTACATTCCACAGGTCAGCTATGCCTCCTCGAGCAGGCTGCTCAGCAACAA CTATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGAGGCCGTTAAGAGGGACATCTGTAT CATAGAGGAGATAAACAGCAGCCCAGCCTTCTTCCCAACTTGACGCTGGGATACAGGAT ATTGACACGTGTAACACCGTGTCCAAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA GECCGAGATCATCGAGCACTTCCAGTGGAACTGGGAACCCTGGCAGCCGACGATGA TGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAGCAGTTGGAGTTCATCGCCGA CTTTCCTATTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAAATCAAGGCCGGAGTC GACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGGCTCCAGGCGATGATATTCGC TGTGGAATGTATCAGGTATAATTTCCGTGGGTTTCCCTGGTTACAGGCTATGATATTTGC AATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCAATATCACCCTGGGATATCGCAT CGICAICCAGAACTCCICGGCCAAGGICAICGIGGICTICICCAATGGCCCCGACCIGGA CTCAGGGTATGGTCCAAACCAAAGGGCCCCAGAAGAAGAAGAGACATCATACTGGGAGGTCT CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTAAAATCGAGACCGGAGGC 17; Length Indels . 9 Match 42.2%; Score 1745.2; DB 6; Local Similarity 76.4%; Pred. No. 7.6e-273; Les 2187; Conservative 0; Mismatches 658; 1023 1161 1083 1221 1143 1203 1341 1281 1263 a ठ व ठ g ò g ò g

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SUMMARIES

	Description	Aad41631 SKCaR DNA	Abk14910 DNA encod	Abl59964 Dogfish s	Adhl0916 Shark pol	Aad64738 Dogfish s	Adil9962 Dogfish s	Aat89290 Dogfish s	Aaz31049 Human CaR	Aax90922 Human cal	Aal43269 Human CaR	Ado29824 Human GPC	Abz42663 Human cal	Abx74489 Human cDN	Aat61382 Parathyro	Aav26964 Human par		Aaz25055 Human par	Aav82485 Human par	Aaz89298 Human cal	Aaf86094 Small hum	Aai72122 cDNA enco	
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ALIGNMENTS

The invention relates to a method for growing marine fish in fresh water. The method involves: adding at least one polyvalent cation sensing receptor (PVCR) modulator to fresh water to modulate or maintain expression and/or sensitivity of at least one PVCR in atleast one tissue; transferring the marine fish to the fresh water, modified according to the previous step; and adding feed containing Nacl to contribute to a significant increased level of the PVCR modulator in serum of the marine fish. The invention is useful for growing marine fish in freshwater e.g. mackerel, pollock, sea base, sword fish, tuna, winter flounder and summer flounder. The marine fish cultured by the method have stronger immune Growing marine fish in fresh water involves adding polyvalent cation receptor modulator and feed containing sodium chloride. in water; polyvalent cation sensing receptor; PVCR; fat content; receptor; ds. Betka M; Harris HW, Russell DR, Nearing J, Disclosure; Fig 14; 71pp; English. .; DNA; 4134 BP. 11-OCT-2001; 2001WO-US031625. 12-OCT-2000; 2000US-00687373. (AQUA-) AQUABIO PROD SCI LLC. invention. st entry) WPI; 2002-394428/42. WO200230215-A2. 18-APR-2002.

	CCTGGCAGCGACGATGACTATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGAGGGGGGGAGGCTAGACACTCCTCAGTACTACACCCAGAAATAACACTCTCAGTACTACACCCAGAAATAACACTCTCAGTACTACACCCAGAAATGACTCTCTCT	TCCAATGGCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGAT 132	1 TTCCACGTGGTCGGCGCACCATCGGCTTCGCTCTCAGGCGGGGCGTATCCCAGGGTTC 144	1 TTCTGGGAGAGACCTTCAACTGCTACTTCACCGAGAGACCCTGAGGCTGAAGAAT 156 1 TTCTGGGAGGAGCCTTCAACTGCTACTTCACCGGGAAGACCCTGACGCTGAGGAGTTT56 1 TCCAAGGTGCCCTCGCACGGCGGCGCTCAAGGGGAAGCTCC 162 1 TCCAAGGTGCCTCGCACGGCGCGCTCAAGGGGACGCTCCAAGGCGGGAACTCC 162 1 TCCAAGGTGCCTCGCACGGACCGGCGGTCAAGGGGACTCC 162	AGACGACAGCCCTACGCCACCCTGCACGGAGGAGGAGAACATGACCACACACA	1741 ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAAACCCGGCACGGGCATCTTTGCAAAC 1800 1741 ATTGCTCACGCCTGCAAGACATCCACTCTTGCAAACCCGGCACGGGCATCTTTGCAAAC 1800 1801 GGATCTTGTGCACATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCGAT 1860 1801 GGATCTTGTGCACATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCAT 1860 1801 GGATCTTGTGCACATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCAT 1860	1861 CTGAAGTTTACCAACAGCATGAGGAGCAGGTTGACTTTGACGATCAAGGTGACCTCCAAG 1920 1861 CTGAAGTTTACCAACAGCATGAGCAGGTTGACTTTGACGATCAAGGTGACCTCCAAG 1920 1921 GGGAACTAACAACTGGCAGGTTGACTTTGACGATGAATCGATTCAT 1980 1921 GGGAACTACCATTATCAACTGGCAGCTTCCCGCAGAGGATGAATCGGTGTTTTCAT 1980 1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCCGCAGAGGATGAATCGGTGTTTCAT 1980 1981 GAGGTGGGCAACTACAACTGCAGCTCTCCCCCAGAGAGATGAATCGATGTTCCAT 1980 1981 GAGGTGGGCAACTACAACGCTAAGCCCAGTGACCAACAACAAAAG 2040
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C functions and are less susceptible to parasitic, bacterial, viral and CC fungal diseases and thus are much healthier. The marine fish are economically produced and have a higher fat content and a milder, less CC fishy taste. The present sequence is SKCaR DNA used to illustrate the CC method of the invention XX SQ Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other; Query Match Best Local Similarity 100.0%; Score 4134; DB 6; Length 4134; Best Local Similarity 00.0%; Pred. No. 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ATTCCGTTGCTGTTCGTTCCTCCTCCTGTGCTGTGTGTGT	GTCATTGTATGA GTCATTGTATGA GTCATTGTATGA GTTCACCTTTCT 	Qy 301 ATGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTACAAAGATAA 360 Db 301 ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTACAAAGATAA 360 Qy 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGCTAGTGTGGCTTAGTCAGGAA 420 Db 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGCTAGTGTGGCTTAGTCAAGGAA 420 Db 361 GCAGAAATCCTCCCAGGCATCCTCTGTAAACGGCTGGCGTAGTGTGGTCAAGGAA 420	QY 421 CAGAGACAGGGCTGCACAATGGCTCACTACTGCCAACTCTTATTCTTGGGATTTACA 480 Db 421 CAGAGACAGGGCTGCACAATGGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480 Cy 481 CTCCTACAGTGGTCTCAGGGTATGGTCCAAAGGGCCCAGAAGAAAGGA 540 Db 481 CTCCTACAGTGGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGAAAGGA 540	Qy 541 GACATCATACTGGGGGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600 Db 541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600 Qy 601 TTAAAATCGAGACCGGAGGGGACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 Db 601 TTAAAAATCGAGACCGAGGGGACAAAAATGTATTCGGTACAATTTTCCAAGGCTTCCGATGG 660	TGATATTCGCAATTCAAGACATTAACAACAGTATGACTTTCCTGCCCAAT	781 ACACTCAGCTTTGTGGCCCAGAACAAAATCGACTCGCTGAACTTAGATGATGATTCTGTAAC 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid sequence (I) encoding a polyvalent cation-sensing receptor protein (PVCR), especially Shark fidney calcium receptor related protein—I (SKCAR-RP-I) that allows fish to sense ion concentrations. The aquatic PVCR allows the successful adaptation of fish, such as flounder, to marine and fresh water environments, and controls maturation and developmental stages in marine species. Modulating the expression of PVCR activates or inhibits PVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. Activating PVCR in epithelial cells increases or decreases salinity tolerance in aquatic species. Regulating salinity tolerance is useful to develop new species of marine fish that are easily adaptable to fresh water aqua culture. The methods are useful for adaptable to fresh water adua culture. The methods are useful for altering body composition e.g. fat content, protein content, weight, thickness, moisture and taste. The species can be maintained in both environments, onsecutively to reduce parasites, bacteria and contentian (Updated on 07-NUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                         "Shark kidney calcium receptor related protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule encoding polyvalent cation-sensing receptor protein, useful for regulating adaptation of fish e.g. flounder to manand fresh water environments, and to alter tissue or meat/muscle
                                                                                                                                    Shark kidney calcium receptor related protein-1; SKCaR-RP-1; polyvalent cation-sensing receptor protein; PVCR, fish; flounder; salinity tolerance; fat content; protein content; weight; fish maturation; fish development; gene; ss; spiny dogfish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;
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                                                                                                    shark kidney calcium receptor related protein-1,
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                         "SKCaR-RP-1"
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439. .3522
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CAGAGACAGGGCTGCACAATGGCTCACTTCACTGCCAACTCTTATTCTTGGGATTTACA
/product= "Dogfish shark kidney
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12-OCT-2000; 2000US-00687476.
12-OCT-2000; 2000US-00687477.
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                                                                                                                                               ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780
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               AGCGGCGACGACCTGCCATCTAGACACCACGACCAGGGCCCGCCTCAGAAATGCGAGCCC
                                                    CAGCCCGCCAACGATGCCCCGATACAAGGCGGCGGCGACCAAGGGCACCCTAGAGTCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fish; polyvalent cation sensing receptor; PVCR; anadromous fish; polyvalent cation sensing receptor modulator; PVCR modulator; feed; atlantic salmon; arctic char; rainbow trout; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dogfish shark kidney cation receptor (SKCaR) DNA SEQ ID NO:17
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The present invention describes a method for improving the raising of pre-adult anadromous fish maintained in fresh water prior to transfer to seawater. The method involves: (a) adding at least one polyvatent cation sensing receptor (PVCR) modulator to the fresh water; and (b) adding a feed containing an agent that increases the level of PVCR modulator in the serum of fish. The PVCR modulator has anabolic activity. The method can be used for improving the raising of pre-adult anadromous fish e.g. salmon, char and trout, maintained in fresh water prior to transfer to seawater. The present sequence encodes doglish shark kidney cation receptor (SKCaR), which is relative to the PVCRs from salmon, char and Improving the raising of pre-adult anadromous fish e.g. salmon involves adding polyvalent cation sensing receptor modulator and a feed containing an agent that increases level of modulator in serum of fish. TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCCATT 301 Arceccarrearcriccaccacricrecreraaccarccricaccarraaacaraa GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGCTGAGGACCAC dricacccrircriggagcaracgarcarccrgaaggagarggaggagacrirgaggaga TATTAAAATGITTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 1 AAITCGGITGCIGTCGGITCAGICCAGAGICTCCCCCAGIGCAAAATGAGAAAIGGIGCIC GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAAGACTTGAGGAGGAA ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTACAAAGATAA AATTCCGTTGCTGTTCAGTCCAAGTCTCCTCCAGTGCAAAATGAGAAATGGTGGTC GCCATTACAGGAACATGCACTACATCTGTGAATGAAATATTGTCAGTTATCTGAAGGT 61 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATCTGAAGGT Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;

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420 480

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120 120

1561 TCCAAGGTGCCCTCGCACGGCGCGCTCAAGGGGACGCTCCAAGGCGGGGAACTCC	1741 ATTGCTCACGCCCTGCAAGACATCCACTTGCAAACCCGGGCACGGGCATCTTTGCAAAC 1800	1921 GGGAACTACACCATTATCAACTGGCAGCACACGAGAGGATGAATCGGTGTTGTTCCAT 1980 1921 GGGAACTACACCATTATCAACTGGCAGCACCCAGAGGATGAATCGGTGTTGTTCCAT 1980 1921 GGGAACTACACCATTATCAACTGCACACCCCAGAGGATGAATCGGTGTTGTTCCAT 1980 1981 GAGGTGGGCAACTACACCACCCAACGCAACACCACACACA		2221 AATGATTTCTGGAATGAGAACCACGTCGTGCATCGCCAAGGAGATCGAGTACCTG 2280 2281 TCGTGGACGAGCCCTTCGGAATCCCTCTGACCACTTCGCCGTACTGGCATCCTGATC 2340 2281 TCGTGGACGAGCCCTTCGGAATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATC 2340 2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGAACACTCCCATCGTGAAGGCCACC 2400 2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGAACACTCCCATCGTGAAGGCCACC 2400 2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGAACACTCCCATCGTGAAGGCCACC 2400 2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGAACACTCCCATCGTGAAGGCCACC 2400 2401 ACCTCCTTCGTGCTGCTGCTTCTTCTCTCTCTTCTTCTTCT	2401 AACCGGGGTTGTCCTACTGCTCTTCTCTCTCTCTGTGTTCTCCAGCTTCTCCAGCTCCTC 2460 2461 ATCTTCATCGGCGAGCCCAGGGACTGGACCTGTCGGCTTCTCGCCACCGGCTTTTGGCATC 2520 2461 ATCTTCATCGGCGAGCCCAGGGACTGGACCTGTCGGCTCCGCCAACCGGCTTTTGGCATC 2520 2521 AGCTTCGTCCTGTGCATCTCTGCATCGGTGAGACCAACCGGGTCTTTGGCATC 2520 2521 AGCTTCGTCCTGTGCATCTCCTGCATCCTGGTGAAAACCAACC
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CAGAGACAGGCTGCACAATGGCTCAGCTT CTCCTACAGTCGTACAATGTCTCAGGGTAT CTCCTACAGTCGTACAATGTCTCAGGGTAT CTCCTACAGTCGTACATGTCTCAGGGTAT GACATCATACTGGGAGGTCTCTTCCCAATA GACATCATACTGGGAGGTCTCTTCCCAATA TTAAAATCGAGACGCGAAGAATGT			961 AddaGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCCCCC	CAGTTG CAGTTG CAGTTG TCCAAT	TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGT TTCCACGCA TTCTCCACGT TTCTCCACGCA TTCTCCACGCA

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ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAGTATTTTTAGTGACA
                                                                                                              TTGCAACAGGAATATAATGACTGTAACAAAAATTGTTGATTATCTTAAAAATGCAAAT
                                          ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA
                                                                                                 TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT
                                                                                                                                                      GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAAACATTTATCATTGAAACCTGGA
                                                                                                                                                                           GACTGAGATTGCCACTGTGATGACAGAACTGTTTTATAAACATTTATCATTGAAACCTGGA
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18-APR-2002; 2002US-00125792.
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                                                                            CTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCATCATCATCACCTGCGAC
                                                                                                                                   GAGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGCTACACCTGCCTCGCCTCGCCGCCATC
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                                                                                                                                                                        TGCTTCTTCTTCGCCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTC
                                                                                                                                                                                       ATCTCCTCGCCCGCCTCGTCCACCTGCGGGCCGGGCTCACCATGGAGATGCAGCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCCGCCAACGATGCCCCGATACAAGGCGCCCGACCAAGGGCCACCTAGAGTCGCCG
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       CTGGTCTTCCTCTGCATCCTGCAAATCGTCACCTGCATCATCTGGCTCTACACCGGG
                                                                                                                 GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGCTACACCTGCCTCGCCGCCCATC
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The invention comprises the amino acid and coding sequences of poly cation sensing receptor (PVCR) proteins from Atlantic salmon. The D protein sequences of the invention are useful in the commercial rai of Atlantic salmon and the restoration of wild Atlantic salmon populations, especially in the transfer from freshwater to seawater increased growth and reduced mortality. The present DNA sequence en a shark PVCR-related protein. Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other; uery Match Local Similarity 100.0%; Score 4134; DB 10; Length 4134; est Local Similarity 100.0%; Pred No. 0; or Thals 0. Garanthes 4134; Conservarive 0. Mismarches	1 AATTCGTTGCTGTCGTTCGTCCAAGTCTCCTCCAGTGCAAATGAGAATGGGGTC 60 1 AATTCGTTGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAATGGTGGTC 60 1 AATTCGTTACAGGACTCAGTCTCAAGTCTCCTCCAGTGCAAATGAGAGTGTC 60 61 GCCATTACAGGAATGACTACATCTGGTTAATGAAATATTGTCAGAGGT 12 61 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATCTGAAGGT 12 61 GCCATTACAGGAACATGCATACATCTGTTAATGAAATATTGTCAGTTATCTGAAGGT 12 121 TATTAAAATGTTCTGCAAGGATGCTTCACGAGAAATCAATTCTCCCACGTTTTCCCATT 18	0 0-0 0-0 4-4		601 TTAAATCGAGACCGACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 601 TTAAAATCGAGACGAGAGAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 601 TTAAAATCGAGACGAGAGAAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 661 CTCCAGGCATGATGAAAGGATTAACAACAGTATTCCAGGCTTCCTGCCCAAT 720 661 CTCCAGGCATGATTCGCAATTGAAAGGATTAACAACAGTATGCCTTTCCTGCCCAAT 720 721 ATCACCCTGGGATATCGCAATTTGACACGTGTAACACGTGTCCAAGGCGTAGAGGCA 780 721 ATCACCCTGGGATATCGCATATTTGACACGTGTAACACGTGTCCAAGGCGTAGAGGCA 780 721 ATCACCCTGGGATATCGCAATTTGACACGTGTAACACGTGTCCAAGGCGTAGAGGCA 780 721 ATCACCCTGGGATATCGCAAATTGACACGTGTAACACGTGTCCAAGGCGTAGAGGCA 780 721 ATCACCCTGGGATATTGACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 840 731 ACACTCAACTTTGTGGCCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 840 731 TGCTCTGACCATATCCCAATAGCAGTGGTCGAGGCAACTGGGGTCAGGAATCTCC 900 841 TGCTCTGACCATATCCCAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC 900 841 TGCTCTGACCATATCCCAAAAACCAAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC 900 841 TGCTCTGACCATATCCCAATAGCAGTGGTCGGGGCCAACCGGGTCAGGAAATCTCC 900
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&	961	AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT	1020
g	196	AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT	1020
ጵ ዴ	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGGAACTGGGGAACTGAACATGAACATGAACATGAACATGAACATGAACATGAACATGAACATGAACATGAACATGAACTAGAACTGAACTGAACTAACATGAACTGAACTAACATGAACATAACATGAACTAACATGAACTAACATGAACTAACATGAACTAACATGAACTAACATGAACTAACATAAC	1080
	1081	ACCTIGGCAGCGACGATGACTATGGCCCCCAGGCATTGACAAGTTCCGGGAGGAGGCC	1140
ą	1081	ACCTGGCGGCGGCGATGATATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGGCC	1140
≿ :	1141	GITAAGAGGAACATCIGTAITGACTICAGIGAGAIGATCICICAGIACTACACCCAGAAG	1200
ი .	1141	GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
& &	1201	CAGTIGGAGTICATCGCCGAGGTCATCCAGAACTCCTCGGCCAAGGTCATCGTGGTCTTC	1260
⋩	1261	TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGGT	1320
ą	1261	TCCAATGGCCCCGGACCTGGGGCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGGT	1320
<i>≿</i> ;	1321	CGGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTATGCCAAGCCAGAGTAC	1380
ą	1321	CGGATCTGGCCAGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTAC	1380
× ×	1381	TICCACGIGGICGGCGCACCATCGCITCGCTCTCAGGCGGGGCGTATCCCAGGGTTC TITCACACGTGTCGCTTCAGGTTCGCTTCAGGCGGGGGGGGTATCCCTAGGGTTC TITCACACGTGTCAGGGTTCAGGGTTCAGGTTCAGGTTCAGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGTTCAGGGTTCAGGGTTTCAGGGTTCAGGTTCAGGGTTTCAGGGTTTCAGGGTTTCAGGTTCAGGTTCAGGTTCAGGTTTCAGGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTCAGGTTTCAGGTTCAGGTTCAGGTTTCAGGTTCAGGTTTCAGGTTCAGGTTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAGGTTTCAG	1440
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× 4	1441	AACAAGTTCCTGAAGGAGGTCCACCCCAGCAGGTCCTCGGAAAGGGTTTGTCAAGGAG A	1500
· >	1501	TTCTGGGAGGAGCCTTCAACTGCTACTTCACGGAGAAGACCCTGACGCAGCTGAAGAAT	1560
ď	1501	TTCTGGGAGGAGCCTTCAACTGCTACTTCACCGAGAAGACCCTGACGAGGAGT	1560
λ;	1561	TCCAAGGTGCCTCGCACGGACCGGCGGCTCAAGGGACGGCTCCAAGGCGGGGAACTCC	1620
ą	1561	TCCAAGGTGCCCTCGCACGGACCGGCGGCTCAAGGGGACGGCTCCAAGGCGGGGAACTCC	1620
λ;	1621	AGACGGACAGCCTACGCCACCCTGCACTGGGGAGAGAAACATCACCAGCGTGGAGACC	1680
ą	1621	AGACGGACAGCCTACGCCACCCTGCACTGGGGAGGAGGAACATCACCAGCGTGGAGACC	1680
۲ ۲	1681	CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC	1740
Q	1681	CCCIACCIGGATTATACACACCIGAGGATCICCIACAA1GIATACGIGGCCGICTACICC	1 /4 C
≿ 1	1741	ATTGCTCAGGCCCTGCAAGACATCCACTCTTGCAAACCCGGCACGGGCATCTTTGCAAAC 	1800
· } ≥	1801	GGATCTTGTGCAGATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCAT	1860
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<u>ک</u>		CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGACTTTGACGATCAAGGTGACCTCAAG	1920
ą	1861	CTGAAGTTTACCAACAGGTGAGGTGAGGTTGACTTTGACGATCAAGGTGACCTCAAG	1920
≿ ;	1921	GGGBACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
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                          GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGCTGAGGACCAC
                                                                                                                                                                                                                                                                                                                                                                            CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGGAAAGGA
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                                                                                                                                                                                                                        GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA
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                                                                                                                                                                  Polyvalent cation-sensing receptor; PVCR; anabolic; homeostatic; shark kidney calcium receptor related protein-I; SKCaR-RP-I; dogfish shark; SKCaR-I; gene; ss.
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27-MAR-1997; 97WO-US005031.
28-SEP-1998; 98US-00162021.
17-NOV-2000; 2000US-00715538.
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Db 2401 ACCTCCTTCGTGCTGGGGGTCTTCATCAGGAACACTCCCATCGTGAAGGCCACC 2400	2581 GAGGCCAACATCCCACCACCACCACGTGGGTGGGCTCCACCTGCACTTCCTC [bb 2641 CTCCTCCAGCTACCTGAAATCGTCACTGCAATCATCATCTGTCACCTGCGG 2700 2641 CTCGTCTCCTCTGGGAACCATCATCATCACCACTCATCTGGCTCTTGACCTGGG 2700 2701 CCTCCCTCCAGCTACAGAACCATGAGTGGAACAACAACATCATCATCATCATCATCACCTGGGA 2760 Db 2701 CCTCCTCCAGCTACAGAACCATGAGTTGATCATCATCATCACCTGCGAC 2760	2761 GAGGGCTCGCTCATGGCCTGGGCTTCCTCATCGGCTACACCTGCCTCCTCGCCGCCATC 2	OY 2821 IGCTTCTTCTCAGCTCCGTAAGCTGCGGAGAACTTCAAGAGCTAAGTTC 2880 Db 2821 IGCTTCTTCTTCACTTCAAGTCCCGTAAGCTGCCGGAGAAACTTCAACGAGGCTAAGTTC 2880 O. 2821 IGCTTCTTCTTCAACTTCAAGTCCCGTAAACTGCGAGAAACTTCAACGAGGCTAAGTTC 2880	2981 ACCACCTACGCAAGTTTGTGTCGGCCGTGGAGGTGATTGCCATCCTGGCTTCGAGCTTC 3	Db 2941 AGCACCTACGGCAAGTTTGTGTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTC 3000 Qy 3001 GGGCTGCTGGGCTTTACTTCAACAAGTGTTACATCCTGTTCAAGCCGTGCCGT 3060	Db 3001 GGGCTGCTGCATTTACTTCAACAAGTGTTACATCATCATGTTCAAGCCGTGCGT 3061 AACACCATCGAGGAGGTGCGCTGCAGCACGAGCGCCCCACGCCTTCAAGGTGGCGGCCCGG 3120 Db 3061 AACACCATCGAGGAGGTGCGCTGCAGCAGCGGCGCCCACGCCTTCAAGGTGGCGGCCCGG 3120	3121 GCCACCTCCGGCGCAGCGCCGCGTCTCGCAAGGCTCCAGCAGCTGTGCGGGTCCACC 3 1121 GCCACCTCCGGCGCGCGCGTCTCGCAAGCGCTCCAGCAGCCTCTGCGGGTCCACC 3	3181 ATCICCTOGCCGCCTCGTCCGCCCGGCCCGGCCTCACATGCAATGCGCGCTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	3241 AGCACGCAGAAGGTCACTTCGGCAGCGGCACCGCTCTCTCT	3301 ACAGGCCGATAGGCCACCTTAGCCGACCGCCGCAGGAGGAGGAGGAGGAGGCGGGGGGGG	3361 AGGGCGACGTGCCATCTAGACACCACGAGGCCCGCCTCAGAATGCGAGCCC 34	Oy 3421 CAGCCGCCAACGATGCCGATACAAGGCGCGCCGACCAACGATGCCG 3480
	1441 AACATHICCTGAAGGACCCCACCCACCTCGGACAATGGCATTGTCAAGGAG 1500 1501 TTCTGGGAGGACCTTCAACTGCTTCACTCCGGAAGAAGACCCTGACGCTGAAGAAT 1560 1501 TTCTGGGAGGACCTTCAACTGCTTCACCTGAAGAAGACCCTGACGCTGAAGAAT 1560 1501 TTCTGGGAGGACCTTCAACTGCTACTTCACCGAAAGAACCCTGACGAGAAT 1560	1561 TCCAAGGTGCCCTCGCACGGCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC 1620 1561 TCCAAGGTGCCCTCGCACGGCGGCTCAAGGGGACCTCCAAGGCGGGAACTCC 1620 1621 AGACGGACACCGCCCCTGCACCTGCACGGGAGAACATCACAGGGGGAACTCC 1680	1621 AGACGGACAGCCTACGCCACCCCTGCACTGGGAGAGACATCACCAGCGTGGAGACC 1680 1681 CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCGTCTACTCC 1740	ATTGCTCACGCC	GGATCTIGTGCAGATATTAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCAT 186	1861 CTGAAGTTTACCAACAGCATGGGTAAGCAGTTGACTTTGACGATCAAGGTGACCTCAAG 1920		1981 GAGGIGGGCAACTACAACGCCTACGCTAAGCCCAGTGACCGACTCAACATCAACGAAAG 2040 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTGGAGTGT 2100 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCCAACTGCAGTGGACTGT 2100	2101 GTGCCGGGCACCAGGAAAGGGATCATCGAGGGGGAGCCCACCTGCTGCTTTGAATGCATG 2160 2101 GTGCCGGGCACCAGGAAGGGATCATCGAGGGGAGCCCACCTGCTTTGAATGCATG 2160	2161 GCATGTGCAGAGGGAGAGTTCAGTGATGAAAACGATGCAGTGCGTGTACAAGTGCCG 2220 	2221 AATGATITCTGGTCGAATGAGAACCACGTCGTGCATCGCCAAGGAGATCGAGTACCTG 2280 2221 AATGATITCTGGTCGAATGAGAACCACGTCGTGCATCGCCAAGGAGATCGAGTACTG 2280	2281 TCGTGGACGCCTTCGGGATCGCTCTGACCATCTTCGCCGTACTGGCCATCCTGATC 2340 2281 TCGTGGACGGAGCCCTTCGGGATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATC 2340	41 ACCTCCTTCGTGCTGGGGTCTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACC

4080 3780 3840 3900 3960 3960 4020 4080 3660 3720 3780 4020 3600 GGCGGCAGCAAGGAGCGCCCCACACTATGGAGGAAACCTAATCCAACTCCTCCATCAAC GGCGGCAGCAAGGAGCGCCCCACAACTATGGAGGAAACCTAATTCCAACTCCTCCATCAAC CCCAAGAACATCCTCCACGGCAGCACCGTCGACACTGACATCAACTCCTAACCGGTGGC CCCAAGAACATCCTCCACGGCACCACGTCGACAACTGACATCAACTCCTAACCGGTGGC TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAAC ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAAGTATCTGAACTATCTGAAGT ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA ATCTGAACTACTTTATTCTCTCTGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT GACTGAGATTGCCACTGTGATGACAGAACTGTTTTATAACATTTATCATTGAAACCTGGA GACTGAGATTGCCACTGTGATGACAGAACTGTTTTATAACATTTATCATTGAAACCTGGA TIGCAACAGGAATATAATGACTGTAACAAAAAATTGTTGATTATCTTAAAAATGCAAAT TIGCAACAGGAATATAATGACTGTAACAAAAAATGTTGATTATCTTAAAAAATGCAAAT TGTAATCAGATGTGTAAAATTGGTAATTACTTCTGTACATTAAATGCATATTTCTTGATA TGTAATCAGATGTGTAAAATTGCTAATTACTTCTGTACATTAATGCATATTTCTTGATA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCCGACAACGG 4134 ere-adust anadromous fish, polyvalent cation sensing receptor; PVCR, stress, dogfish shark; gene; ds. /*tag= a /product= "Dogfish shark SKCaR protein" Dogfish shark kidney cation receptor (SKCaR) DNA Location/Qualifiers BP ADI19962 standard; DNA; 4134 2003US-00410872 12-OCT-2000; 2000US-00687372 (first acanthias. US2003230247-A1 09-APR-2003; 15-APR-2004 18-DEC-2003 3661 3841 3901 4021 4081 3481 3541 3541 3601 3601 3661 3721 3781 3781 3841 3901 3961 3961 4081 3481 3721 Squalus 엄 õ 원 상 원 8 6 6 6 8 8 g 9 9 ò dd ò g ò g

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The present invention relates to methods for improving the raising of pre-adult anadromous fish or preparaing these fish for transfer to seawater by modulating expression of a receptor referred to as the Polyvalent Cation Sensing Receptor (PVCR). The invention is useful in increasing survival and growth and reduce stress of the fish that have been transferred to seawater. The present sequence is a dogfish shark cation receptor (SKCaR) DNA.
                                                                                                                                                                             Growing pre-adult anadromous fish in freshwater comprises adding feed containing an amount of NaCl for fish consumption to the freshwater to increase the level of the Polyvalent Cation Sensing Receptor modulator serum of the fish.
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100.0%; Pred. No. 0;
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12-OCT-2000; 2000US-00687476.
12-OCT-2000; 2000US-00687477.
11-OCT-2001; 2001US-00975553.
11-OCT-2001; 2001WO-US031562.
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Matches 4134; Conservative
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P-PSDB; ADI19970.
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8 8 8	1 CICCAGGCGATGATACTGCCAATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCAATTAACACCGTGTCCCAAGGGGGGTTAGAAGGGGGATTAGAGAGGGGATAATTGACAGGGGGGGG	ço qa	1801 GGATCTTGTGCAGATATTAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCAT 1860
8 8 8	21 ATCACCCTGGGGATATCGCATATTTGACACGTGTAACACCGTGTCCAAGGGGGCGCGCTGAACTTTGTGGGCCCAGAACAAATGGACTCGCTGAACTTAGATGAGT.	oy do	1861 CTGAAGTTTACCAACAGGGGGGGGGGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
3 & 2	TGCTCTGACCATATCCCACCAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC 90	රි ව	1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCAT 1980
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8 & 8	01 ACCUIGGCAGGCGACGAIGACTAIGGCCGCCCAGGGAITGACAGIICCGGGAAGGAGGCC 114 41 GTTAAGAGGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 120 61	λ _ο α	2221 AATGATTTCTGGTCGAATGAGAACCA.GCGTCGTGCATCGCCAAGGAGATCGAGTACCTG 2280
3 & 2	GITAGGAGGACATCIGANIGACIICANIGAGATGATCATCATGAGATCANAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	Q DP	2281 TCGTGGACGGAGCCTTCGGGATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATC 2340
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8 & 8	1 CCANTIGGECCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGTCGGAGAGAAAACATCGGTTCACCGATTTCAGGCCAGGCGAGGCTTTCGCTCATTGCCAAGCCAGGGGTTACTTTCGTTCATTGCCAAGCCAGAGTACTTACT	% q	2401 AACCGGGAGITGTCCTACTGCTGCTGTCTCCCTCATCTGCTGCTTCTCCAGCTCGTC 2460
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8 & 8	1 TTCCACGTGGTCGGCGG 1 AACAAGTTCCTGAAGGA 1	do Op	2521 AGCTTGGTCCTGTGCATCTCCTGGTGAAGACCAACCGGGTGCTGCTGGTGGTCTTC 2580 2521 AGCTTCGTCCTGTGCATCTCCTGCTGAAGACCAACCGGGTGCTGCTGGTGATC 2580
3 & 1	441 AACAAGIICCIGAAGGAGGICCACCCAGCAGGICCICGGACAAIGGGIIIGICAAGGAG 1 501 TTCTGGGGAGGACCTTCAACTGCTACTTCACCGAGAAGACCCTGAGGCAGCTGAAGAAT 1	상 원	2581 GAGGCCAAGATCCCCACCAGCCTCCACCACAAGTGGGTGG
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성 음	1 TCCAAGGTGCCCTCGCACGGACGGCGCTCAAGGGGGACGGCTCCAAGGCGG 1 AGACGGACAGCCCTACGCCCTGCACTGGGGAGGAGAACATCACCAGCG	<i>`</i> 8	2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCATCTTCATCATCACCTGCGAC 2760
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27-MAR-1996; 8 6 5 g g d ે ò 3180 3180 3240 3240 3300 3300 3360 3360 3420 3420 3480 3480 3540 3540 3600 3600 3660 3660 3780 3900 3000 3060 3120 3120 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAAC 3720 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAAC 3720 AICTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA 3840 TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT 3900 GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGCTACACCTGCCTCCTCGCCGCCATC 2820 GGCGGCAGCAAGGAGCGCCCCACAACTATGGAGGAAACCTAATCCAACTCCTCCATCAAC 3541 CCCAAGAACATCCTCCACGGCAGCACCGTCGACAACTGACATCAACTCTAACCGGTGGC ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT ALCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGAC ATCACCTTCAGCATGTTGATCTTCTTCATGGTCTGGATCTCCTTCATCCCCGCCTATGTC 3001 GGGCTGCTGCGCTTTACTTCAACAAGTGTTACATCATCTGTTCAAGCCGTGCCGT 3061 AACACCATCGAGGAGGTGCGCTGCAGCACCACGCGCCCCACCCTTCAAGGTGGCGGCCCGG GCCACCCTCCGGCGCAGCGCCGCGTCTCGCAAGCGCTCCCAGCAGCCTGTGTGCGGCTCCACC AGCACGAGAAGGTCAGCTTCGGCAGCGGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG 3241 AGCACGCAGAAGGTCAGCTTCGGCAGCGGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG ACAGGCCGATACGCCACCCTCAGCCGCACGCCCGCAGCAGCAGCAGCAGCGGGGATGGCCGC AGCGGCGACCACCTGCCATCTAGACACCACGACCAGGGCCCGCCTCAGAAATGCGAGCCC CAGCCCGCCAACGATGCCCGATACAAGGCGCGCCGACCAAGGGCACCCTAGAGTCGCCG CAGCCCGCCAACGATGCCCGATACAAGGCGGCGCGACCAAGGGCACCTAAGAGTCGCCG TGCCCAACCTCTCCCGCCACTTTGCGTTTTGCTGAAGATTGCAGCATCTGCAGT TGCCCAACCTCTCCCCGCACTTTGCTTTTGCTGAAGATTGCAGCATCTGCAGT 2821 TGCTTCTTCGCCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTC 2881 ATCACCTTCAGCATGTTGATCTTCATCGTCTGGATCTCCTTCATCCCCGCCCTATGTC GGGCTGCTGGGCTGCATTACTTCAACAAGTGTTACATCATCATCAAGCCGTGCCGT AACACCATCGAGGAGGTGCGCTGCAGCACGGCGCCCACGCCTTCAAGGTGGCGGCCCGG GCCACCCTCCGGCGCGCCGCGCGTCTCGCAAGCGCTCCAGCAGCTGCGGCTGTGCGGCTCCACC 3181 ATCTCCTCGCCCGCCTCGTCCACCTGCGGGCCGGGCCTCACCATGGAGATGCAGCGCTGC <u> ACAGGCCGATACGCCACCCTCAGCCGCACGCCCCGCAGGCAACTCGGCGGATGGCCGC</u> AGCGGCGACGTGCCATCTAGACACCACGACCAGGGCCCGCCTCAGAAATGCGAGCCC GOOGGCAGCAAGGAGCGCCCCACAACTATGGAGGAAACCTAATGCAACTCCTCCATCAAC CCCAAGAACATCCTCCACGGCAGCACGTCGACAACTGACATCAACTCCTAACCGGTGGC 2941 3121 3241 3361 3361 3421 3481 3661 3721 3721 3781 3841 2941 3301 3301 3421 3481 3541 3601 3601 3661 3781 3841 2761 2881 3061 2821 3001 3121

4020 GACTGAGATTGCCACTGTGATGACAGAACTGTTTTATAACATTTATCATTGAAACCTGGA TTGCAACAGGAATATAATGACTGTAACAAAAAATTGTTGATTATCTTAAAAATGCAAAT TTGCAACAGGAATATAATGACTGTAACAAAAAATTGTTGATTATCTTAAAAATGCAAAAT TGTAATCAGATGTGTAAATTGGTAATTACTTCTGTACATTAAATGCATATTCTTGATA GACTGAGATT 3901 4021 3901 3961 3961 4021

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AAT89290 standard; cDNA; 4131

AAT89290;

(first entry)

Dogfish shark kidney calcium receptor related protein cDNA

Calcium receptor related protein; CaR-RP; dogfish shark; SKCaR-RP; polycation-sensing receptor; aquaculture; fish farming; salinity tolerance; ss.

Squalus acanthias.

Location/Qualifiers 439. .3519 /*tag= a 4076. .4113 /*tag= b polyA_site Key

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Hebert S; Brown E, Harris HW,

WPI; 1997-489640/45. P-PSDB; AAW32059.

New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity tolerance of fish for use in aquaculture.

Claim 2; Fig 4A-F; 57pp; English.

This cDNA clone codes for dogfish shark kidney calcium receptor related protein (SXCaR-RP, see AAW32059), an aquatic polyvalent cation-sensing receptor (PVCR). It was isolated from a shark kidney colvant library using a rat kidney calcium receptor CDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP sequence; an isolated PVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for aquatic PVCR activates or inhibits aquatic PVCR mediated ion transport and endocrine changes

TGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCC	961 AGCAGGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGG	1021	1081	1141 1141	1201 CAGTIGGAGTICATGGCGGACGTCATCCAGAACTCCTCGGCCAAGGTCATCGI 	Qy 1261 TCCAATGGCCCGGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAAACATCA(D)	Oy 1321 CGGATCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGTACCAGAGTACAGGAGTACCAGAGTACCAGAGTACAGGCCAGCCA	OY 1381 TICCAGGGGGCACCATCGCTTCGCTCTCAGGGGGGGGGGG	OY 1441 AACAAGTTCCTGAAGGAGGTCCACCAGGAGGTCCTCGGACAATGGGTTTGTCAAGGAG 1441 AACAAGTTCCTGAAGGAGGTCCA-CCCAGCAGGTCCTCGGACAATGGGTTTGTCAAGGAG	Qy 1501 TTCTGGGAGGACCTTCAACTGCTACTCACGAGAAGACCTGACGCAGCTGAGGATAAT	OY 1561 TCCAAGGTGCCTCGCACGGACCGGCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC	Qy 1621 AGACGGACACCCTACGCCACCCTGCACTGGGGAGGAGAACATCACCAGCGTGGAGACC Db 1618 AGACGGACACCCTACGCCACCCCTGCACTGGGGAAGAACATCACCACGCTGGAGGACACACCCAGCGTGAACACCACCCTGGAGAACAACATCACCAGCGTGAACACACCACCCTGCACCACCCCTGCACCACCCCTGCAACAACAACATCACCAACCA	Qy 1681 CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTC	Qy 1741 ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAAACCGGCACGGCACGGCATCTTTGCAAAC Db 1738 ATTGCTCACGCCCTGCAACATCCACTCTTGCAAACCCGGGCACGGGCATCTTTGCAAAC	Qy 1801 GGATCTTGTGCAGATATTAAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	Qy 1861 CTGAAGTTTACCAACAGGAGGAGGAGGTGACTTTGACGATCAAGGTGACCT Db 1858 CTGAAGTTTACCAACAGGATGAGGTGAGCTTGACTTTGACGATCAAGGTGACCT	Qy 1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGTTGTTCCTCTCTCT	Qy 1981 GAGGTGGGCAACTACAACGCCTACGCTAAGCCCAGTGACCTCAACATCAACATCAACAAAG Db 1978 GAGGTGGGCAACTACAACGCCTAAGCCCAATGACCGACTCAACATCAACGAAAG
that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of	ne fish that are easily adaptable to fresh water aquacultur nnce 4131 BP; 1028 A; 1161 C; 1019 G; 923 T; 0 U; 0 Other;	ery Match st Local Similarity 99.9%; Pred. No. 0; tches 4131; Conservative 0; Mismatches 0; Indels 3; Gaps 3;	1 AATICCGIIGCIGIGGGIICAGICCAAGICICCICCAGIGCAAAAIGAGAAAIGGIGGIC 60	61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 	TATTAAAATGTTTCTGCAAGGATGGCTTCACGGGAAATCAATTCTGCACGTTTTCCCATT 1	GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGGTGAGGACCAC 2	1 GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGAAGGAAG	ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGGGATCCCTCACCATTACAAAGATAA 3	GCAGRATICTCCAGGCATCCTCTAAACGGCCTGCCTAGTGCCTTGGTCAAGGAA 4	21 CAGAGACAGGGCTGCACAATGGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 48	CONTRACTOR	41 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 60 [TAAAATCGAGACCGAGCGACAAAATGTATTCGGACAAATTTTCGAGCTTTCGATGG 66 TTAAAATCGAGACCGAGCGACAAAATGTATTCGGACAATTTTTCGAGCCTTTCGATGG 6 TTAAAAATCGAGACCGAAGCGAAAATGTATTTTTTTTTT	CTCCAGGGGATGATATTGGCAATTGAGAGATTAACAAGAGTATGACTTTCCTGCCCAAT 72	ATCACCCTGGGATATCGCATATTTGACACGTGTAACACCGTGTCCAGGCGCTAGAGCG 78	ACACTCAGCTTTGTGGCCCAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 84	/81 ACACICAGEINIGIGGCCCAGGACAAAAICGACTICGCIGAACITAGATGAGITCIGIAAC 840 841 TGCTCTGACCATATCCCATCCACAATAGCAGTGGTGGGGGGAACCGGGTCAGGAATCTCC 900 641 TGCTCTAACCATATTGCAATAGCAGTTGCTGCTGCTGCAACTCAATAGCAATCTCC 900	ACGGGGGGCCATCTATCATCATTATTACATTCATCACACACA

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411 TACGATTGCTGTGGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAATCTGCT 470
171 TGTGGAATGTATCAGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to G-protein fusion receptors (I) comprising: (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and intracellular (ICD) domains, each choice in the N to C direction, each choice in Gepencially from a CaR calcium receptor), GluR (derabotropic glutamate receptor) and GABABR (admin-aminobutyric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the Clinker. (I), and recombinant chimeric receptors (RR) without the GP component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act or identify compounds (e.g. allosteric modulators, e.g. stroke, head or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, allows associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, allowers and depression. Nucleic acid (II) that encodes (I) is used: (I) for recombinant production of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of CaR and mGluR domains cells used in screening for modulators. Use of CaR and mGluR domains allows presentation of GABABR domains, to a binding agent, in a form more like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling different domains, ceeptors, lacking one to more domains. By shuffling different domains, ceeptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially useful e.g. for treating or preventing stroke or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 CTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGAAAGGAGACATCATACTGGGAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                              G-protein fusion receptor, CaR, calcium receptor; GluR, head injury; metabotropic glutamate receptor; GABABR; chimeric receptor; stroke; gmama-aminobutyric acid receptor; allosteric modulator; antagonist; spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia; Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garrett JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1745.2; DB 2; Length 3234;
Pred. No. 5.8e-300;
0; Mismatches 658; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3234 BP; 739 A; 931 C; 829 G; 735 T; 0 U; 0 Other;
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Best Local Similarity 76.4%;
Matches 2187; Conservative
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                                                            Human CaR coding sequence.
                                                                                                                                                                                                     cognitive disorder; ss
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Best Local Similarity
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                                                                    The present sequence is the human calcium receptor nucleic acid sequence. This is used in assaying for compounds modulating GABABR activity. GABAB receptors are metabotropic receptors that modulate synaptic transmission in brain. Portions of calcium receptor are swapped with portions of GABABR2 to create protein fusions. The agonist extracellular binding domain is swapped for measurement of antagonist activity. Intracellular domains are swapped for measurement of antagonist activity intracellular different receptor.
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                                                                                                                                                                                                                                                 Gaps
           Novel nucleic acids, used to screen for specific modulators, e.g. treating spasticity or Alzheimer's disease.
                                                                                                                                                                                                                     Score 1745.2; DB 2; Length 3234;
Pred. No. 5.8e-300;
0; Mismatches 658; Indels 17;
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ء <	1341	GGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTACTTCCACGTGGTCGGCGGCAC 1400
ı >-	0	ATCGGCTTCGCTCTCAGGGGGGGGGTATCCCAGGGTTCAACAAGAGGAGGT 146
Д	951	
ρ. κ	1461	ACCTTCAA 152 ACATTTAA 107
۰. ج	1521	TITCACCGAGAAGACCCTGACGCAGCTGAAGAATTCCAAGGTGCCCTCGCACGG 158
3 >	58	SCALCICARANAGGISCARANGACTITACCIGIGAGACTATICS IN COCCACACACCCTACACA 16
, д	12.	
> 4	1641	TATACACA 17
· >	70	CTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCCATTGCTCACGCCCTGCAGA 176
۵	1239	3ATATCCTACAATGTGTACTTAGCAGTCTACTCCATTGCCCACGCCTTGCAAGA 129
> 4	1761	Ø 10
. >-	N -	TGAGGCCTGGCAGGCCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT 188
۵	1359	
۵ خ	1881	GGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAGGGGAACTACACCATTATCAA 1940
>	94	CGGTGTTGTTCCATGAGGTGGGGAACTACAACGC 200
د ۵	2001	TGGCACCTURCCCCAGAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTAAAGGT TACGCTAAGCCCAGTGACCGACTCAACATCAACGAAAAAGAAATCCTCTGGAGTGGCTT 206
, <u>a</u>	53	
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) >	2 2	TCATCGAGGGGGAGCCCACCTGCTGCTTTGAATGCATGGCATGTGCGAAGGGAGGAGTT 218
۰. ۵	65	71
>-	2181	CAAGTGCGTGTACAAAGTGCCCGAATGATTTCTGGTCGAATGA 22.
۵	1719	ccasisccistacaastscccasarsactrerssersatsa 177
> .c	2241	CCTGTCGTGGAC
>-	30	TCGCCGTACTGGGCATCCTGATCACCTCCTTCGTGCTGGGGGT 236
۵	1839	
	;	

2361 CTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACCAACCGGGAGTTGTCCTACCT 2420

à

88; gene; ss GABABR;

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The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of GaR, mGluR and GABABR for use in treating associated conditions. The present cDNA sequence was used in the production of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crirccrarrcarringgagragcagcraaagarcaagarcrcaaarcaaggccggagrc
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                                                                                                                                                                                                transmembrane domain; intracellular domain; modulator identification.
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The invention relates to human and mouse G protein-coupled receptors of GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR polynucleotides of the invention. The invention iturther discloses variants of the GPCR polysphides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of discression, diabetic neuropathy, disorders (e.g., Alzhainer's disease, disorders of the adrenal gland; disorders (e.g., Alzhainer's disease, disorders of the adrenal gland; disorders (e.g., Alzhainer's disease, distrathoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., augina, cardiac arrhythmia or mycocardial infarction); muscular disorders (e.g., auctions or intestine consensation relaxemia); immune disorders (e.g., auctions); cardiovascular disorders (e.g., auctions); cardiovascular disorders (e.g., auctions); cardioters (e.g., auctions); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stonach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR encoding context disorders of the kidney, liver, lung, breast, ovary, check the invention. Note: The full sequence data for this context belown were obtained in the commence of the prince descent directly from WIPO at the laws of the propertical directly from sequences.
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42.2%; Score 1745.2; DB 12; Length 3237;
Best Local Similarity 76.4%; Pred. No. 5.8e-300;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; C
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Transgenic mouse; neurological disorder; adrenal gland disorder;

Colon disorder; intestinal disorder; adrenal gland disorder;

Transgenic mouse; neurological disorder; adrenal disorder;

Muscular disorder; blood disorder; immune disorder; bone disorder;

Midney disorder; inter disorder; nutritive disorder; cancer;

W voary disorder; uterus disorder; prostate disorder; testis disorder;

Skin disorder; thyroid disorder; prostate disorder; spleen disorder;

Transgenic; antiinflammatory; vasotropic; antidarhoeic; antidabetic;

Vircide; hepatotropic; antibarcerial; antialarmoeic; antidabetic;

W dermatological; antibacterial; antialarmoeic; antidabetic;

W dermatological; antibicer; antibrichyroid; antialarmicer; numan;

mmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
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                                                                                                                                                                                    CACCTGCGGGCCGGGCCTCACCATGGAGATGCAGCGCTGCAGCACGCAGAAGGTCAGCTT 3260
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Zeng H;
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Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GPCR CASR polynucleotide, SEQ ID NO:926.
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Madisen L, Mcilwain KL, Pavlova MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO29824 standard; cDNA; 3237 BP
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osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABS42523 to ABZ42569 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                           Sequence 3783 BP; 892 A; 1067 C; 975 G; 849 T; 0 U; 0 Other;
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        CATCAGCAGCAAGCAACA----GCGAAGACCCATTCCCACAGCCCGAGAGGAGGA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor medulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; ALS, cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; albergy; osteoperosis; cardiomyopathy; inflammation; osteoarthritis; allergy; osteoperosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                        COGCAGCOCACCOTCACCCTGTCOCTCAGCTTCGAGGACAGGCCGATACGCCACCCT
                                                                                                                                                  CAGCAGCAGCCGCTGGCCCCTAACCCAGCAAGAGCAGCAGCAGCAGCAGCCCCTGACCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human calcium sensing receptor nucleotide SEQ ID NO:117.
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2481 GARCICACTOCTACCTCCACCACCCCCTCCCCTCCCTCCTCCTCCTCCCCCC	RESULT 13 ABX74489 ID ABX74489 XX XX AC ABX74489; XX DT 21-MAR-2003 (first entry) XX DE Human cDNA sequence #32 down-regulated in CC-RCC patients.
1341 GGCTTGGGCCAGCTCTCCGCTCATTGCCAAGCCAGAGTCTTCCAGGTGGTTGGCGGCACC 1302 1263 GGCTTGGGCCAGCTCTCCCCCTATTCCCAAGCTTCTCAAGTCTTCCAGGTGGTTGGCGGCACC 1212 1264 GGCTTGGCTCTCCAGGCCGCGCGCGTTCCCAGGTTTCCAAGTTCTCCAGGTGGTTGGT	2301 GATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATCACCTCCTTCGTGCTGGGGGT 2360 [

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                                                                                                                                                                                                                                                     New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.
        Human; microarray; solid surface; immobilised probe; CC-RCC; differential expression profile; aggressive CC-RCC tumour type; olear cell renal carcinoma; ene expression profiling; cumour tissue; gene; ss.
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Ouery Match 42.2%; Score 1745.2; DB 10; Length 3783; Best Local Similarity 76.4%; Pred. No. 6e-300; Matches 2187; Conservative 0; Mismatches 658; Indels 17;
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/note= "Pages 94-95 are missing from the specification,
sequence information was obtained from the EPO"
                                                                                                                                              CACCTGCGGGCCGCCCTCACCATGGAGATGCAGCGCTGCAGCACGCAGGAAGGTCAGCTT
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using pBopCaR1 as a hybridisation probe. mRNA was isolated from a 39 year clones of approx. 5 and 4 kb were identified. These oblnA's were injected inco Xenopus ocytes which were assayed for the presence of functional calcium receptors as assessed by the stimulation of calcium-activated chloride currents upon addition of appropriate calcium receptor agonists. WPS currents upon addition of appropriate calcium receptor agonists, of the existence of at least two sequence variants differing in the 3' untranslated region and which may result from alternative upoxyadenylation. Sequence analysis of the two cDNA clones indicated untranslated region and which may result from alternative transcription initiation and/or splicing. Three additional sites of transcription initiation and/or splicing. Three additional sites of sequence variation occur within the coding regions of cDNA clones phuepcaR5.2 and phuepcaR6.0 splicing. Three additional substance analysis of the human can gene indicates that the additional 30 bp in clone phuepcaR5.2 as compared to phuepcaR4.0, results insert 10 additional amino acids into the CaR protein encoded by thuepcaR5.2 between residues 536 and 537 of the protein encoded by thuepcaR5.2 between residues 536 and 537 of the protein encoded by thuepcaR5.2 between residues 536 and 537 of the protein encoded by thuepcaR5.2 between residues 536 and 537 of the protein encoded by thuepcaR5.2 between residues 536 and 537 of the protein encoded by the positions. These two receptor isoforms may be functionally and/or these positions. These two receptor isoforms may be functionally and the manacologically distinct

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Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T; 0 U; 0 Other;

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Best Local Similarity 76.4%;
Matches 2187; Conservative 501 423 561 483 621 543 681 741 663 861 921 981 903 1101 à d ò g ò QQ ò g ò 셤 ò D ò ВÞ ò g δ 셤 ઠે 셤

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The Human parathyroid calcium receptor gene encodes a 1078 amino acid protein. The tissue from which the receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates alters through changes in Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ hose in Ca2+ homeostasis in Ca2+ hose in ca2+ hose in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium recombinantly, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise an tibodies for use in detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                         concentration; parathyroid hormone; homeostasis; kidney;
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42.2%; Score 1745.2; DB 2; Length 3809;
Best Local Similarity 76.4%; Pred. No. 6e-300;
Matches 2187; Conservative 0; Mismatches 658; Indels 17;
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3362
                                                       3226 cadcadecanetreadeadeadeceaandeaadeadaad 3267
                                                                                                                                                                                                                                                                                                                                                                                                    Human parathyroid calcium receptor 4.0 gene 4Kb fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "pHuPCaR 4.0 4Kb fragment"
                                                                                                                                                                                                                    AAV26964 standard; cDNA to mRNA; 3809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium receptor; detection.
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/*tag= a
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CTCAGGGGATATGGGCGAAAGGCCCAGAAAGGAAAGAAAG	

qq	2571	CATGCAGATIGICATCIGIGIGAGTCIGGCTCTACACCGCGCCCCCCTCAAGCTACCGCAA 2630
ò	2721	CCATGAGCTGGAGGACGAGGTCATCTTCATCACCTGCGACGAGGGCTCGCTC
qq	2631	CCAGGAGGAGGAGGATGATCTTCATCACGAGGCCACGAGGGCTCCCTCATGGCCCT 2690
ò	2781	GGGCTTCCTCATCGGCTACACTGCCTCCTCGCCGCCATCTGCTTCTTCTTCGCTTCAA 2840
qq	2691	GGGCTICCTGATCGGCTACACCTGCTGCTGCTGCTATCTTCTTCTTTGCCTTCAA 2750
ò	2841	GICCCGTAAGCIGCCGGAGAACTICAACGAGGCTAAGTICAICACCTICAGCAIGITGAI 2900
Db	2751	GICCCGGAAGCTGCCGGAGAACTICAATGAAGCCAAGTICATCACCTICAGCATGCTCAT 2810
ò	2901	CITCHTCATCGTCTGGATCTCCTTCATCCCCGCTATGTCAGCACCTACGCAAGTTTGT 2960
QQ	2811	CITCTICATCGTCTGGATCTCCTTCATTCCAGCCTATGCCAGCACCTATGGCAAGTTTGT 2870
ò	2961	GTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTCGGGCTGCTGCATTTA 3020
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ò	3021	CITCAACAAGTGITACATCATCTGTTCAAGCCGTGCCGTAACACCATCGAGGAGGTGCG 3080
Ωþ	2931	CTTCAACAAGATCTACATCATTCTTTCAAGCCATCCCGCAACACCATCGAGGAGGTGCG 2990
ò	3081	CTGCAGCACGGCGGCCCACGCCTTCAAGGTGGCGGCCCGGGCCACCCTCCGGCGCAGCGC 3140
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ò	3141	CGGGTCTCGCAAGGGCTCCAGCAGCTGCGGCTCCACCATCTCCTCGCCCCCTCGTC 3200
qq	3051	GETCTCCCGCAAGCGGTCCAGGCGCTTGGAGGCTCCACGGGATCCACCCCCCTCCTCCTC 3110
λõ	3201	CACCTGCGGGCCGGGCTCACCATGGAGATGCAGCGCTGCAGCAGCAGAGAGGTCAGCTT 3260
Db	3111	CATCAGCAGCAAGAAGCACAGCGAAGACCCATTCCCACAGCCCGAGAGGCAGAAG 3165
ઠે	3261	CGGCAGCGGCACCGTCACCTGTCGCTCCAGGAGACAGGCCGATACGCCACCT 3320
οp	3166	CAGCAGCAGCCGCTGGCCCTAACCCAGCAGCAGCAGCAGCAGCCCCTGACCCTCCCA 3225
ŏ	3321	CAGCCGCACGGCAGCAGGAACTCGGCGGATGGCCGCAG 3362
QQ	3226	CAGCAGCAACGATCTCAGCAGCCCAGATGCAAGCAAG 3267
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28 1703.6 41.2 5006 2 US-08-943-986-2 Sequence 2, Appli 30 1703.6 41.2 5006 3 US-08-943-986-2 Sequence 2, Appli 31 1703.6 41.2 5006 3 US-08-484-159-2 Sequence 2, Appli 32 1703.6 41.2 5006 3 US-08-484-159-2 Sequence 2, Appli 33 1678.2 40.6 4131 1 US-08-484-159-1 Sequence 2, Appli 34 1678.2 40.6 4131 1 US-08-484-565-4 Sequence 4, Appli 35 1678.2 40.6 4131 2 US-08-484-565-4 Sequence 4, Appli 36 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 4, Appli 36 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 4, Appli 37 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 4, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 4, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 6, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 6, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 6, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 6, Appli 40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 7, Appli 40 1678.2 40.0 4 US-09-435-897-2 Sequence 2, Appli 40 111.4 26.9 2925 4 US-08-697-2894-1 Sequence 1, Appli 40 17.2 3384 2 US-08-687-289A-1 Sequence 1, Appli 40 17.2 3384 2 US-08-687-289A-1 Sequence 1, Appli
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Sequence 1, Application US/09162021B
Fatent No. 637391
GENERAL INFORMATION:
APPLICANT: H. William Harris
APPLICANT: Edward M. Brown
TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
TITLE OF INVENTION: Species and Methods of Use Thereof
TITLE OF INVENTION: Species and Methods of Use Thereof
FILE REFERENCE: 2856.1001-007
CURRENT APPLICATION NUMBER: US/09/162,021B
FRIOR PAPLICATION NUMBER: PCT/US97/05031
PRIOR PAPLICATION NUMBER: PCT/US97/05031
PRIOR PLING DATE: 1998-09-28
PRIOR PLING DATE: 1998-03-27
PRIOR FILING DATE: 1996-03-27
PRIOR FILING DATE: 1996-03-27
PRIOR FILING DATE: 1996-03-27
PRIOR FILING DATE: 1996-03-77
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; Pred. No. 0;
0; Mismatches
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100.0%;
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Best Local Similarity 100.
Matches 4134; Conservative
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Page 3

Db 3541 CCCAAGAACATCCTCCACGGCAGCACCAACAACTGAACTCCTAACCGGTGGC 3600 Qy 3601 TGCCCAACCTCTCCCTCTCCGGCACTTTGCTTTTGCTGAAGATTGCAGCATCTGCAGT 3660 Bb 3601 TGCCCAACCTCTCCCCTCTCCGGCACTTTGCTTTTGCTGAAGATTGCAGCATCTGCAGT 3660 Qy 3661 TCCTTTTATCCCTCTCTCCGGCACTTTACTAGTGTGCGATGCACTTTCAAACTTTACTAGTTTACTAGTGAATATCACAAC 3720 Bb 3721 ATAATGACTTTATCGCAACTTTTACTAGTTACTAGTGAACTATCTGAAGT 3780 Qy 3721 ATAATGACTTATTCTCGAATTGTTACTAGTTGTCTAACTATCTGAACTATCTGAAGT 3780 Qy 3721 ATAATGACTTATTCTCCCAATTGTTACTAGTGAACTATTTACTAACTA	OY 3941 TTATGTTCTAACATTGTCAAGATAATTGTTACAACATATAAGGTACCACCTGAAGCAGT 3900 3941 TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACCTGAAGCAGT 3900 OY 3901 GACTGAGATTGCCACTGTGAATGAACACGTTTATAAACATTTATCATTGAAACCTGCA 3960 Db 3901 GACTGAGATTGCCACTGTGATGAACACATTTATAAATTTATTAACATTTAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAAA	RESULT 2 US-09-687-477-17 is gequence 17, Application US/09687477 is general INFORMATION: is APPLICANT: Aurais, H. William, Jr. is APPLICANT: Russell, David R. is APPLICANT: Russell, David R. is APPLICANT: Becka, Marles is TITLE OF INVENTION: Rish is TITLE OF INVENTION: Rish is TITLE OF INVENTION: Rish is CURRENT APPLICATION NUMBER: US/09/687,477 is CURRENT FILING DATE: 2000-10-12 is NUMBER OF SEQ ID NOS: 23 is SOFTWARE: FastSEQ for Windows Version 4.0 is LENGTH: 4134 is TYPE: DNA	y Okcarism: Dogitsh Shark US-09-687-477-17 US-09-687-477-17 US-09-687-477-17 100.0%; Score 4134; DB 4; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY AATTCCGTTGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAATGGTGGTC 60 Db AATTCCGTTGCTGCGGTTCAGTCCAAGTCTCCTCCAGTGCAAAATGAGTCTC 60 QY AATTCCGTTGCTGCTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAAATGAGTCTC 60 QY GCCATTACAGGAACATGCACTACATCTGTTAAATGAAAATGTCAGTTATCTGAAAGT 120
ATCTTCATCGGCGAGCCCCAGGGACTGGACCTGTCGGCCCAACCGGCCTTTGGCATC	CTCCCTCCAGGTACAGGAACCATGAGGTGGAGGACGAGGTCAT AGGGCTCGCTCATGGCCTGGCTTCCTCATCGGCTACACGTCCT AGGGCTCGCTCATGGCCTGGGCTTCCTCATCGGCTACACCTG AGGCTCCTTCATGGCCTTCGTGCTCTCTCTCTCTCTCTCT	AACACCATCGAGGGGGGCGCGCGCGCGCGCGCGCGGGGGGGG	3361 AGGGGGAGACTGCATCTAGACACAGGGCCGCCTCAGAATGCGAGACCC 3420 3361 AGCGGCGACGACCTGCATCTAGACACACAGGCCCGCCTCAGAATGCGAGCCC 3420 3421 CAGCCCGCCAACGATGCCGATACAAGGCGCGCCGACCAAGGGCACCCTAGAATGCGAGCCC 3420 3421 CAGCCCGCCAACGATGCCCGATACAAGGCGCCCGACCAAGGGCACCCTAGAGTCGCCG 3480 3421 CAGCCCGCCAACGATGCCCGATACAAGGCGCCCGACCAAGGGCACCCTAGAGTCGCCG 3480 3481 GCCGGCAACAAGAGGCGCCCAACACTATGGAGAAACCTAATCCAACTCTCCATCAAC 3540 3481 GCCGGCAACAAGAGGCCCCCACAACTATGGAGAAACCTAATCCAACTCCTCCATCAAC 3540 3541 CCCAAGAACATCCTCCACGGCACCCCCACAACTGACAACCTCAACCCCTTAACCGATCAAC 3500

1311 AGCCGGGAGAGCACCACCACCACCACCACCACCACCACCA	RESULT 3 US-09-687-476-17 i Sequence 17, Application US/09687476 j Pacent No. 6475792 j GENERAL INFORMATION: APPLICANT: Harris, H. William, Jr. APPLICANT: Harris, H. William, Jr. APPLICANT: Betka, Marlies for Raising Pre-Adult Anadromous TITLE OF INVENTION: Fish TITLE OF INVENTION: Fish TITLE OF INVENTION: Fish ITILE REFERENCE: 2213.2001-000 CURRENT APPLICATION NUMBER: US/09/687,476 CURRENT FILING DATE: 2000-10-22 NUMBER OF SEQ ID NOS: 23 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17 LENGTH: 4134 TYPE: DNA ORGANISM: DOGSISH Shark
TCSTGGACGCCCTTCGGGAACCCTTCACCACTTCGCCGTACTGGGCATCCTGATC 2281 TCSTGGACGCCCTTCGGGAACCTCTCACCCTTCTCGCCGTACTGGGCATCCTGATC 2281 TCSTGGACGCCTTCGGGAACCTCTCACCCTTCTCCCTTCTCTCTC	3061 AACACCATCGAGGAGGTGCGCTGCAGCCCCCCCCCCCCGG 3120 3061 AACACCATCGAGGAGGTGCGCTGCAGCCCCCCGG 3120 3121 GCCACCTCCGGCGCCTCTGCAGCCCCCCCCCTCTCAGGTGCGCCCCGG 3120 3121 GCCACCTCCGGCGCCGCGTCTCGCAGCGCTCCAGCGCTCTGCGGTCCACC 3180 3121 GCCACCTCCGGCGCGCGCTCTCGCAGCGCTCCAGCAGCTCTGCGGTTCCACC 3180 3121 GCCACCTCCGGCGCGCGCTCTCGCAGCGCTCCAGCAGCTCTGCGGTTCCACC 3180 3181 ATCTCCTCGCCCGCTCTCCCCCCGCGGCTCCACCAGCAGCTCCACGAGATGCAGCGCTCCACC 3240 3181 ATCTCCTCGCCCGCTCTCCGCGGCGCGCTCCACCATCGAGATGCAGCGCTGC 3240 3241 AGCACGCCGCTCGTCCGCGGCGCGCGCGCGCGCCCTCACCATCGAGAGGGGCGCTCCACCATCGAGAGGGGGGGG

783-00-211	7-425-12		
Ouerv	100,0%; Sco	ò	1021 GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTAGGA 1080
t Lo ches	ocal Similarity 100.0%; Pred. No. 0; 5 4134; Conservative 0; Mismatches 0; Indels 0	g 8	JAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGGGAGT TTGCCAACTCGACCATGACTTATGGCCTCAGGCATTTGACAAAGTGGAACT
දු පු	1 AATTCCGTIGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAAATGAGAAATGGTGGTC 60	7 d	ACCCTGGCAGCCGACGATGACTATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGAGGAGGCC 114
S S	61 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATCTGAGGT 120 	oy Op	GTTAAGAGGGAATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 120
ζς Dp	121 TATTAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT 180	දු දු	
ò f	1 GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGTGAAGACCAC 	oy D	1261 TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGGT 1320
1 & a	1 GTTCACCCTTTCTTGGAGATACGATCACCCTGAAGGAGATGGAAGACTTGAGGAGGAAAAAAAA	o, d	1321 CGGATCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTAC 1380
\ \ \ \ \	1 AIGGGGATTGAICTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTACAAGATAA AIGGGGATCCCTCACCATTACAAGATAA AIGGGGATCCCTCACCATTACAAGATAA AIGGGATTAATCAATCAATCAATACAAGATAAA AIGGGATTAACCAAGGATAA	ò d	1381 TTCCACGTGGTGCGCGCACCATCGCTTTCGCTCTCAGGGGGGGG
ે જે ક	GCAGAAATCCTCCAGGCATCCTCTGTAAACGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 	SP GS	1441 AACAAGTTCCTGAAGGAGGTCCACCCCAGGAGTCCTCGGACAATGGGTTTGTCAAGGAG 1500
3 % 4	CAGAGACAGGCTGCACATGCTCACTTCACTGCCAACTCTTATTCTTGGGATTTACA [දු පු	1501 TTCTGGGAGGACCTTCAACTGCTACTTCACCGAGAAGACCCTGACGCGCGCTCAAGAAT 1560
g & g	CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCCAAACCAAAGGGCCCAGAAGAAGAACTCTTCTACAGTCTACAGTCTCAGGGTATGGTCCAAACCCAAAGGCCCCAGAAAAGGA	è d	GCCCTCGCACGGACCGGGGCTCAAGGGGACGGCTCCAAGGCGGGGAACTCC 162
& &	GAČATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGA 	පු දු	168 168
\$ 65 26	TTAAAATCGAGACGGAGGGACAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 66	oy Oy	CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC 17
ÇQ QQ	61 CTCCAGGCGATGATATTCGCAATTGAACAGATTAACAACAGTATGACTTTCCTGCCCAAT 72	QY Dp	CCTGCAAGACATCCACTCTTGCAAACCGGGCAGGGGTCTTTGCAAAC 18
S S S	21 ATCACCCTGGGATATCGCATATTTGACACGTGTAACACCGTGTCCAAGGCGCTAGAGGCA 7	QV Dp	GGATCTIGIGCAGATATTAAAAAGTIGAGGCCTGGCAGGTCCTCAACCATCTGCTGCAT 1
ò q	ACACTCAGCTTTGTGGCCCAGAACAAATGGCTTGCTGAACTTAGATGACTAAAATCGACTGAACTTAGATGAACAAAATCGACTGAACTTAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTAACT	SP GS	1861 CTGAAGTTTACCAACAGGATGGGTGAGGTTGACTTGACGATCAAGGTGACCTCAAG 1920
ò	TGCTCTGACCATTCCCATCCACAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC 90	Qy Db	1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCAT 1980
ે જે ક	ACGCTGTGGCCAATCTATTGGGATTATTTAACATTCCACAGGTCACCTATGCCTCCTCG	oy Bp	1981 GAGGTGGGCAACTACAACGCTACGCTAAGCCCAGTGACCGACTCAACATCAACGAAAAG 2040
1 & A	AGCAGGCTGCTGAGCAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT 1	상 옵	2041 AAAATCCTCIGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCGAGACTGT 2100

1311	APPLICANT: Russell, David R. APPLICANT: Nearing, Jacqueline
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
	FICCGGCGCGCCGCGTCTCGCAAGCGCTCCAGCAGCCTGTGCGGCTCTCTGCGGCTC

FOOT CO-CO-CO OT AOM DIT

	ICANT: Betka, Marlies 5 OF INVENTION: Methods for Raising Pre-Adult Anadromous	8	TOACCATATCCCATCCACAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCT
	, ;	<u>8</u>	
	NAT APPLICATION NUMBER: US/09/687,372 NAT FILING DATE: 2000-10-12	λο	901 ACGGCTGTGGCCAATCTATTGGGGATTATTTTACATTCCACAGGTCAGCTATGCCTCCTCG 960
	SOFTWARE BALSEQ for Windows Version 4.0 SEQ ID NO 17	d d	-6
	LENGTH: 4134 TYPE: DNA ORGANISM: Dogfish Shark	\chi_	961 AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT 1020
US-09-68' Query ! Rest 14	00.0%; Score 4134;	, Q	1021 GAGCAACAGGCCATGGCCGACATCATCGAGACTTCCAGTGGAACTGGGT 1080
Matche	0; Mismatches 0; Indels C	8 8	ACCTGGCGCGCGATGACTATGGCCGCCCAGGCATTGACAAGTTCCGGGAGGAGGAGGCC 114
රු පු	1 AATTCCGTIGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAATGAGAAATGGTGGTC 60	, q ₀	
à t	GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT	හි සි	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGACATGATCTCTCAGTACTACACCCAGAAG 1200
3 & 3	21 TATTABATGTTTCTGCAAGGATGGCTTCACGAGAATCAATTCTGCAGCGTTTTCCCATT 18	रुं व	1201 CAGITIGGAGITCALGGCGACGICATCCAGAACTCCTCGGCCAAGGICATCGIGGICTTC 1260
90 %	121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT 180 181 GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGGTGAGGACCAC 240	δλ	TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAACATCACCGAT 132
QQ	181 GICATIGIATGAATAACTGACCAAAGGATGTAACAAAATGGAACAAAGCTGAGGACCAC 240	දු දු	TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCGGAT 132
දු දු	241 GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAAGACTTGAGGAGGA 300 	g cá	1321 GGGATCTGGCTGGCCGGGGGGTTGGGCCGGTCTTGGCTGATGCCGGGGTGC 1380 1321 GGGATCTGGCTGGGCGAGGCTTGGGCCGGCTGTTTGGCTGAGGCGAGGTGT 1380
જે તે	AIGGGGAITGAICTICCAGGAGIICIGCIGIAAAGCGAICCCICACCAITACAAAGAIAA	Q.	1381 TTCCACGTGGTCGGCGCACCATCGGCTTCAGGGCGGGGCGGGC
3 8 8	GCAGAAATCCTCCAGGCATCCTGTGAAAGGGGGTGGCGATCCCTTACAAGATAA 38 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGGCTTGGTCAAGGAA 42	ò q	1441 AACAAGTTCCTGAAGGAGGTCCACCCCAGGAGGTCCTCGGACAATGGGTTTGTCAAGGAG 1500 1441 AACAAGTTCCTGAAGGAGTCCACCCCAGCAGGTCCTCGGACAATGGGTTTGTCAAGGAG 1500
o v	301 GCAGARAICCICCAGGCAICCICIGIAAACGGGCIGGCGIAGIGIGGCIIGGICAAGGAA 420 421 CAGAGACAGGGCIGCACAATGGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480	oy d	1501 TTCTGGGAGGAGCCTTCAACTGCTACTTCACCGAGAAGACCCTGACGCAGCTGAAGAAT 1560
දු ර	421 CAGAGACAGGGTGCACAATGGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480 481 CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAAGAA	λō	TCCAAGGTGCCCTCGCACGGACCGGCGCGCTCCAAGGGGGACGGCGACTCC 162
2 40	CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGCCCAGAAGAGA	a 6	1 TCCAAGGTGCCTTGCTACTACTACTACTCAAGGGACGGCTCAAGGGGGGGAAATTC 162
۸۶ م	541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGAC 600	à a	1621 AGACGGACACCCTACGCCACCCTGCACTGGGGAGGAGAACATCACCAGGGGGAGAACATCACCGGGGAGACATCACCGGGGAGAGACATCACCGGGGAGGAGAACATCACCGGGGGAGGAGAACATCACCGGGGGAGAGAACATCACCGGGGGAGAGAACATCACCGGGGGAGAGAACATCACCGGGGGAGAGAACATCACCGGGGGAGAGAACATCACCGGGGAGAGAACATCACCGGGGAGAGAACATCACCGGGGAGAGAACATCACCAGCGGGAGAGAACATCACCAGCGGGAGAGAACATCACCAGCGGGAGAGAACATCACAGCGGGAGAGAACATCACAGCGGAGAGAACATCACAGGGAGAGAACATCACAGGGAGAGAACATCACAGGGAGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAACATCACAGGAGAGAACATCACAGGAGAGAACATCACAGGAGAACATCACAGGAGAACATCACAGAGAACAACAACAACAACAACAACAACAACAACAAC
i & t	TTAAAATCGAGACGGAGAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG	λό q	1681 CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACC 1740
a &	601 TIAAAATCGAGGCGACGACGACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 661 CTCCAGGCGATGATATTCGCAATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCAAT 720	ð í	ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAACCCCGGCCACGGCCATCTTTGCAAAC 180
qq	661 CTCCAGGCGATGATATTCGCAATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCCAAT 720	g è	1/41 ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAAACCCGGCACGGGCATCTTTGCAAAC 1800 1801 GGGACGGGGCATCTTTGCAAAC 1800
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Oy , Db	781 ACACTCAGCTTTGTGGCCCAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 840 	Oy QD	1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920

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Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	q a	541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
	S da	601 TTAAAATCGAGACCGAGAAAATGTATTCGGTAAAATTTTCGAGCTTCCGATGG 660
; Sequence 17, Application US/09975553 ; Patent No. 6564747 ; General Information Information Ur.	& A	661 CTCCAGGCGATGATATTCGCAATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCAAT 720-
	\	21 ATCACCTGGGATAICGCATAITIGACACGIGIAACACCGIGICCAAGGCGCTAGAGGCA 78
us for Kaising-001	G &	1 ACACTCAGCTTTGTGGCCCAGAAATCGACTCGCTGAACTTAGATGATTGAT
; CURRENT APPLICATION NUMBER: US/09/975,553 ; CURRENT FILING DATE: 2001-10-11 : PRIOR APPLICATION NIMBER: 04/687.477	qu	CTTAGAT
PRIOR FILING DATE: 2000-10-12; PRIOR APPLICATION NUMBER: 09/687,476; PRIOR FILING DATE: 2000-10-12	ે લ	841 TGCTCTGACCATATCCCATCACAATAGCAGTGGTGGGGGCAACCGGGTCAGGAATCTCC 900
	B 6	901 ACGCTGTGGCCAATCTATTGGGATTATTTACATTCCACAGGTCAGCTATGCCTCCTCG 960
; SEQ ID NO 17 ; LENGTH: 4134 ; TYPE: DNA ; ORGANISM: Dogfish Shark	\$ 9	961 AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGAT 1020
100.08;	λō	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGG
0; Indels	අධ	GAGCAACAGGCCCACGGCCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGG
Oy 1 AATTCCGTTGCTGTCGSTTCAGTCCAAGTCTCCAGTGCAAATGAGAAATGGTGGTC 60	<u>8</u>	1081 ACCCTGGGAGCCGACGATGACTATGGCCGCCCAGCCATTGACAAGTTCCGGGAGGAGGACC 1140 1081 ACCCTGGCAGGACGACGATGACTATGGCCGCCCAGGCATTGACAAGTTCGGGAGGAGGAGGACGT 1140
61 GCCATTACAGGAACATGCACTACATCTCTCCCCAGGCAAATGAGAAATGGCAAGGTGGTGGTCCCCCCCGCCAGGAAATGTGCAGTAATCTGAAGGT 12	& 43	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCGGAAG 1200
61 GCCATTACAGGAACAIGCACTACATCTGTGTTAATGAAAIATTGTCAGGTTATCTGAAGGT 12 121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT 18	8 &	1201 CAGITGGAGITCATCGCGACGTCATCCAGAACTCCTCGGCCAAGGTCATCGTCGTCGTCTC 1260
121 TATTAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGFTTCCCATT 1 181 GTCATTGTATAACTGACCAAAGGGATGTAACAAATGGAACAAAGCTGAGGACCAC 2	8 &	1261 TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAACATCACCGAT 1320 1261 TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACGAT 1320
181 GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGGAACAAAGAAGGGGCGCAC 241 GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAAGACTTGAGGAGGAA [ò 8	1321 CGGATCTGGCTGGCGAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTAC 1380
241 GITCACCCITICTICGAGCATACGATCAACCCIGAAGGAGATGGAAGACATGAGGAGAGGA	ò 8	1381 TICCACGIGGICGCGCACCAICGGCTICGCTCTCAGGGGGGGGGG
Db 301 ATGGGGATTGATCTTCCAGGAGTTCTGCTGAAAGCGATCCCTCACCATTACAAAGATAA 360 Qy 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGCGTGGCGTAGTGTGGTCAAGGAA 420	ço Op	1441 AACAAGTTCCTGAAGGAGGTCCACCCAGCAGGTCCTCGGACAATGGGTTTGTCAAGGAG 1500
421 CAGAGACAGGCTGCAGATGCTTCAGTGCCGACTTTATTCTTGGGATTTACA 48	8 G	1501 TTCTGGGAGGACCTTCAACTGCTACTTCACCGAGAAGACCCTGACGAGGAGTTAACTT 1560
421 CAGAGACAGGGCTGCACAATGGCTTCACTGCCCAACTCTATTCTTGGGATTTACA 481 CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAACGAAAGGGCCCAGAAGAAAGGA	ò 8	1561 TCCAAGGTGCCCTCGCACGGCGCGCTCAAGGGAACGGCTCCAAGGGGGAACTCC 1620
DB 481 CICCTACAGICGTACAAIGICICAGGGIAIGGICCAAACCAAA	QV	1621 AGACGGACACCCCTACGCCACCCCTGCACTGGGGAGGACATCACCAGCGTGGACACC 1680 1621 AGACGGACAGCCTACGCCACCCCTGCACTGGGGAGAGAACATCACCAGCGTGGAGACACC 1680

2761 GAGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TCCTTTTAICCCTGATTTCTGACTTGGATATTACTAGTGTGCGATGGAATATCACAAC ATAATGAGTTGCACAATTACGTGGATATTACTAGTGTGCGATGGAATATCTGAAC ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT ATCTGAACTTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGAACT ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTTAGTGAACAACATTTTAGTGAACAACATTTTAGTGAACAACATTTGAAGTATTTTTAGTGAACAACATTTGAACTATTTTAGTGAACAACATTTAAGTGAACAACATTTAAGTGAACAACATTTAAGTGAACAACATTTAAGTGAACAACAATTAAAGAACAATTTAAGTGAACAACAATTAAAGAACAATTTAAGTGAACAACAATTAAAAGAACAATTAAAAGAACAATTAAAAGAACAATTAAAAAGAACAACAAAAAAAA
3 8 5 8 6	6 8 8 8 8 8
CCCTACCTOGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC CCCTACCTGGATTATACACACCTGAGGATCTCTCTAATGTATACGTGGCCGTCTTTCTACTCC ATTGGCCGCCCTCCACACACTTTTGCAAACCCGGGCACGTTCTTTTGCAAACCCGGGCACCTTTTTGCAAACCCGGGCACCTTTTTTTT	2581 GAGGCAAGATCCCACCACCACCACGCAAGTGGGTGGCCTCAACCTGCAGTTCCTC 2640 2581 GAGGCCAAGATCCCCACCACCACCACCAGTGGGCTCAACCTGCAGTTCCTC 2640 2581 GAGGCCAAGATCCCCACCACCACCACCAGTGGGCTCAACCTGCAGTTCTCC 2640 2641 CTGGTCTTCCTCTGCATCCTGGTGCAAATCGTCACCTGCATTCATCTGGCTCTACACCGCG 2700 2641 CTGGTCTTCCTCTGGTGCAAATCGTCACCTGCATCATCTGGCTCTACACCGCG 2700 2701 CCTCCCTCCAGCTACCAGGAACCATGAGTGCACCACCACCTGCGACCTGCGCC 2760 2701 CCTCCCTCCAGCTACAGGAACCATGAGTGGAACGAGGACCATCATCATCACCTGCGAC 2760 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAACCAGAGTCATCTTCATCACCTGCGAC 2760 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAACCAGAGGTCATCTTCATCACCTGCGAC 2760

		ACCTGGCAGCCATGGCCGCCCAGGCATTCCAGTGGAACTGGGGAACTGGGGAACTGCGGGAACTGGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAACTGCGGGAAGCCCCGGCCCGGGCCCCGGGCCCGGGCCCTGGCGCCTTGCCGGGAGGCCCCTGGCGCCGCCGCCCGGAGGCCCTGGCGCCTTTGCCTGGAACTCTCGGAACTCTCAGTGAACTCTCAGAAGTTAACTAGAACTCATCAGAACTCTCAGAACTCTCAGAAGTTAACTAAC
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	5	6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
Db 3841 TTATGTTCTAACATTGTTACAACATATAAGGTACCACTGAAGCAGT 3900 3901 GACTGAGATTGCCACTGTGACAGAACTGTTTATAACATTTATCATTGAAACCTGGA 3960 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCATTGAAACCTGGA 3960 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCATTGAAACCTGGA 3960 3901 TTGCAACAGGAATATAATGACTGTAACAAAAAAAAAAAA	RESULT. Sequence 17, Application US/10270795 Sequence 17, Application US/10270795 Sequence 17, Application US/10270795 Patent No. 6637371 PAPPLICANT: HARIS, H. William, Jr. APPLICANT: Haris, H. William, Jr. APPLICANT: Reseal, David R. APPLICANT: Nearing, Jacqueline TITLE OF INVENTION: Fish FILE REFREENCE: 2213.2002-00 CURRENT APPLICATION NUMBER: US/10/2/0,795 CURRENT FILING DATE: 2000-10-12 NUMBER OF SEQ ID NOS: 23 SSOFWARE: FastSEQ for Windows Version 4.0 SSOFWARE: FastSEQ for Windows Version 4.0 SSOFWARE: PastSEQ for Windows Version 4.0 TUPE DNA TU	Query Match 100.0%; Score 4134; DB 4; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; 0; Indels 0; Gaps 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY IATTCCGTTGCTGGTTCAGTCCAGTCCAGTCCAAAGGAAATGACAATGCTGGTC 60 GCATTACAGGAACATGCACTACAGTCTTAATGAAATGTCAGATATCTGAAGGT 120 Db 61 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 Db 62 GCCATTACAGGAACATGCACTACATCTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 QY 121 TATTAAAATGTTTCTGCAAGGATGCTTCACGAGAAATCAATTGTCAGTTATCCCATT 180 QY 121 TATTAAAATGTTTCTGCAAGGATGGATGAACAAAATGAACAAATGGAACAAAGCTGAGGACCAC 240 QY 181 GTCATTGTATGAATAACTGACCAAAGGGATGAACAAAATGGAACAAAGCTGAGGACCACCAAAGGGATGAACAAAGGAACAAAAGGAACAAAAGAAAAAAAA

STTCTGCAAGGATGGCTTCAC TGAATAACTGACCAAAGGGATG	241 GTTCACCTTTCTTGAGGATCGATCAACCTGAAGGAGATGGAAGACTTGAGAGAGA	61 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 4 6 1	421 CAGAGACAGGGCTGCAATGGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480	481 CTCCTACAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGAAGGA 540		601 TTAAAATCGAGACCGGAGGCGACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 	661 CTCCAGGCGATGATATTCGCAATTGAAGACATTAACAACAGTATGACTTTCCTGCCCAAT 720 	721 ATCACCTGGGATATCGCATATTTGACACGTGTAACACCGTGTCCAAGGCGCTAGAGGCA 780	781 ACACTCAGCTTTGTGGCCCAGAACAAATCGACTGGCTGAACTTAGATGAGTTCTGTAAC 840	941 IGCICIGACCATAICCCATCCACAATAGCAGTGGTCGGGGCAACCGGGTCAGGAATCTCC 900	901 ACGGCTGTGGCCAATCTATTGGGATTATTTACATTCCACAGGTCAGCTATGCCTCCTCG 960	961 AGCAGGCTGCTCAGCAACAAGAATGAGTACAAGGCCTTCCTCAGGACCATCCCCAATGAT 1020	1021 GAGCAACAGGCCACGGCCAAGATCATCGAGGCACTTCCAGTGGAACTGGGTGGG	1081 ACCTGGCAGCGAGGAGATATGGCGCCCAGGCATTGACAAGTTCCGGGAGGAGGCCC 1140	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200 	1201 CAGTIGGAGITCATCGCCGACGTCATCCAGACTCCTCGGCCAAGGICATCGTGGTCTTC 1260
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72 72 78	Db 3721 ATAATGAGTTGCACAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780 Qy 3781 ATCTGAACTACTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA 3840 Db 3781 ATCTGAACTATTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA 3840	AGCAGT 390 AGCAGT 390	ACCTGGA 396 ACCTGGA 396	OY 3961 TIGCAACAGGAATATAAFGACTGTAACAAAAAATTGTTGATTATGTTAAAAATGCAAAT 4020 		Qy 4081 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaagcggccgacacgacg	RESULT 7 US-10-270-876-17 ; Sequence 17, Application US/10270876	; Patent No. 6655318 ; GENERAL INFORMATION: ; APPLICANT: Aquablo Product Sciences, LLC ; APPLICANT: Harris, H. William, Jr.	; APPLICANT: Russell, David R. ; APPLICANT: Nearing, Jacqueline ; APPLICANT: Betka, Marlies ; TITLE OP INVENTION: Methods for Raising Pre-Adult Anadromous	; TITLE OF INVENTION: Fish ; FILE REFERENCE: 2213.1004-000 ; CURRENT APPLICATION NUMBER: US/10/270,876 ; CURRENT FILING DATE: 2002-10-11		; SEQ ID NO 17 ; LENGTH: 4134 ; TYPE: DNA ; ORGANISM: Dogfish Shark	17 100.0%; Score 4134; DB 4; Length 4134; imilarity 100.0%; Pred. No. 0;	Sometive	1 AATTCCGTTGCTGTCGGTTCCAAGTCTCCTCCAGTGCAAATGAGAAATGGTGGTC 60 61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATTGAAGGT 12	Db 61 GCCATTACAGGAACAIGCACTACATCTGTGTTAATGAAATATTGTCGTTATCTGAAGGT 120 Qy 121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAATCAATTCTGCACGTTTTCCCATT 180 [

2341 ACCTCCTTCGTGCTGGGGGTCTTCATCAAGTTCAGAAACACTCCCATCGTGAAGGCCACC 2400 	2401 AACCGGGAGTTGTCCTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2461 ATCTTCATCGGCGAGCCCCAGGGACTGGACCTGTCGGCTCCGCCAACCGGCCTTTGGCATC 2520 2461 ATCTTCATCGGCGAGCCCAGGGACTGGACCTGTCGGCTTCGGCTATGGCATC 2520	rgcrggrcrrc 258 rgcrggrcrrc 258	2581 GAGGCCAAGATCCCCACCAGCCTCCACGCAAGTGGGTGGG	2641 CTGGTCTTCCTCTGCATCCTGGTGCAAATCGTCACCTGCATCATCTGGCTCTACACGGG 2700 2641 CTGGTCTTCCTCTGCTGGTGCAAATCGTCACCTGCATCATCTGGCTCTACACGGG 2700	CTTCATCACCTGCGAC 276	2761 GAGGGTTGGCTCATGGGGTTTCCTCATCGGCTACACCTGCCTCCTCGCCGCCATC 2820 2761 GAGGGTTCGTCATGGCGTTCCTCATCGGCTACACTGCCTTCCTCGCCGCCATC 2820	2821 TGCTTCTTCTTCGCCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTC 2880 2821 TGCTTCTTCTTCGCCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTC 2880	2881 ATCACCTTCAGCATGTTGATCTTCTTCATCGCTGGATCTCCTTCATCCCGCCTATGTC 2940 1	2941 AGCACCTACGCAAGTTTGTGTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTC 3000 2941 AGCACCTACGGCAAGTTTGTGTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTC 3000	3001 GGGCTGCTGGGCTTTACTTCAACAAGTGTTACATCATCCTGTTCAAGCCGTGCCGT 3060	3061 AACACCATCGAGGAGGTGCGCTGCAGCAGCGGCGCCCACGCCTTCAAGGTGGCGGCCCGG 3120	3121 GCCACCTCCGGCGCAGCGCCGTCTCGCAAGCGCTCCAGCAGCCCTGTGCGGCTCCACC 3180	3181 ATCTCCTCGCCCCCCTGTCCACCTGCGGGCCGGGCCTCACCATGGAGATGCAGCGCTGC 3240 111	3241 AGCACGCAGAAGGTCAGCTTCGGCAGCGCACCGTCACCCTGTCGCTCTCGAGGAG 3300 3241 AGCACGCAGAAGGTCAGCTTCGGCAGCGCACCGTCACCTGTCGCTCCAGCTTCGAGGAG 3300	3301 ACAGGCGGTACGCCACCCTCAGCCGCACGCGCGCAGCAGCAGCAGCGGGATGGCCGC 3360	3361 AGCGGCGACCACCCATCTAGACACCACGACCCGGCCCGCCTCAGAATGCGAGCCC 3420	3421 CAGCCCGCCAACGATGCCCGATACAAGGCGGCGCCGACCAAGGGCACCTAGAGTCGCCG 3480
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1261 TCCAATGGCCCCGACCTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGAT 132	TCCAATGGCCCCGGAGCCGCTGCAGGCGCTCAGGAGATAGTTCGGGGAAACATCACCGAT 132 CGGATCTGGCCGGCGAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGGGTAC 138	1321 CGGAICIGGCIGGCCAGGGGAGGCCAGGCCAGGCICIICGCCAGGGGGGCGGGGGGGG	1381 TICCACGIGGICGCCGCACCATCGGCITCCCICTCAGGGCGGGGCG	1501 TTCTGGGAGGAGACTTCAACTGCTACTTCACCGAGGAGGCCTGACGCAGGCAG	1561 TCCAAGGTGCCTCGCACGGACTCAAGGGACGCTCCAAGGCGGGAACTCC 162 1561 TCCAAGGTGCCTCAAGGAACTCCAAGGCGAACTCC 162 1561 TCCAAGGTGCCTCAAGACTCAAGGCGAACTCC 162	1621 AGACGGACAGCCCTACGCCCTGCACTGGGAGGAGAACATCACCAGCGTGGAGAC 168 1621 AGACGGACAGCCCTACGCCCTTGCACTGGGGAGAACATCACCAGCGTGGAACAC 168	1681 CCCTACCTGGATTATACACACCTGAGGATCTCCTACAATGTATACGTGGCCGTCTACTCC 174 1681 CCCTACCTGGATTTATACACCTGAGGATCTCCTACAATGTAATACATGGCGTCTAATACC 174	1 ATTGCTCACGCCTGCAAGACATCCACTTGCAAACCCGGCACGGGCATCTTTGCAAAC 180	1801 GGATCTTGTGCAGATATTAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCATT 1801 GGATCTTGTGCAGATATTAAAAAGTTGAGCCTGGCAGGTCCTCAACCATCTGCATT 1 1801 GGATCTTGTGCAATTAAAAAATTGAGGCCTGGCAGGTCCTCAACCATCTGCATT 1 1801 GGATCTTGTGAACAAAAAAAAAAAAAAAAAAAAAAAAAA	1861 CTGAAGTTTACCAACGATGGGGGAGGTTGACTTGACGATCAGGTGACCTCAAG 192 1861 CTGAAGTTTACCAACAGATGGGTGAGGAGGTTGACTTTGACGATCAAGGTGACCTCAAG 192 1861 CTGAAGTTTACCAACAGATGAGGAGGTGAACTTTGACGATCAAGGTGACCTCAAG 192	1921 GGGAACTACACCATTATCAACTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCAT 1	1921 GGGGAACTACACLAITAICAACTGGGAAGAGGAAGAGGATGAATGGGTGTGTTCAT 1981 1981 GAGGTGGGCAACTACACGCTAAGGCCAAGAGTGACCGACTCAACATCAACGAAAAG 204 1981 GAGGTGGGCAACTACAACTAACACTAAAGAGTGACCGACTCAACACATCAACAAAAAAG 204 1981 GAGGTGGGCAACTAAAAAAAAAAAAAAAAAAAAAAAAAA	2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTGTTTCTCCAACTGCAGTGTTTCTCCAACTGCTTTTCTCCAAGTGTTTCTCCAAGTGTTTCTCCAAGTGTTTCTCCAAGTGTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTC	2101 GTGCCGGCCACCAGGAAGGGGATCATCGAGGGGAGCCCACCTGCTGCTTTGAATCCATG 216	2161 GCATGTGCAGAGGAGAGTTCAGTGATGAAACGATGCAAGTGCGTGTACAAAGTGCCG 222	2221 AATGATTICTGGTCGAAGGAACCACGTCGTGCATCGCCAAGGAGATCGAGTACTG 228	2281 TCGTCGACCCTTCGGCATCGCTTCACCATCTCCCCAACCAA	

Ouery Match Dest Local Similarity 100.0%; Score 4134; DB 4; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; O; Indels O; Gaps O; Matches 4134; Conservative O; Mismatches O; Indels O; Gaps O; QY	OY 121 TATTAAANGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT 180 121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAAAATCAATTCTGCACGTTTTCCCATT 180 OY 181 GTCATTGTATGAATAACTGACCAAAGGGATGTAACAAAATGAAAAAGGAACAAAAGGAACAAAGGAACAAAGGAACAAAGGAAAAAA	Db 241 GTTCACCCTTTCTTGAGGATTCTTCTTGAGGAGATTCTTTTTTTT		661 661 721 721 721 781 961 961
Db 3421 CAGCCGCCAACGATACAAGGGGGCGCGACCAAGGACCCTAGAGTCGCG 3480 Qy 3481 GGCGGCAAGGAAGGACCCCCAAACTATGGAAAACCTAATCCAACCATCAACAAGTCGCCG 3480 Db 3481 GGCGGCAAGCAAGGAACTATGGAGAAACCTAATCCAACTCCTCCATCAAC 3540 Qy 3541 CCCAAGAACATCCTCCACGCACACTATGGAGAAACTTCATCCTAACCGGTGGC 3600 Db 3541 CCCAAGAACATCCTCCACGGCACACAACTATAACTCATCAACTCCTAACCGGTGGC 3600 Qy 3541 CCCAAGAACATCCTCCACGGCACCACTATCAACAACATTCAACTCCTAACCGGTGGC 3600 Qy 3601 TGCCCAACCTCTCCCCGGCACTTTGCTTTTGCTCAACACTTCTGCAGT 3600	Db 3601 TGCCCAACTTCTCGGCACTTTGCGTTTTGCTGAAGTTGCAGCATCTGCAGT 360 Qy 3661 TCCTTTTATCCCTGATTTTCTGACTTTGCTTTTACTAGTGGCGATATCCAAC 3720 Db 3661 TCCTTTTATCCCTGATTTTCTGACTTTGATTTTACTAGTGTGCGATGGAATATCACAAC 3720 Qy 3721 ATAATGAGTGACTTGGCTGGAGTATCTGAAGTATCTGAAGT 3780 Db 3721 ATAATGAGTTGCACAATTAGGTGAGCAGAGTATCTGAAGT 3780 Db 3721 ATAATGAGTTGCACAATTAGGTGAGCTGCTGAAGTATCTGAAGT 3780 Dc 3721 ATAATGAGTTGCACAATTAGGTGAGCTGTGTGTCTCAAAGTATCTGAAGT 3780 Dc 3721 ATAATGAGTTGCACAATTAGGTGAGCTGTGTGTCTCAAAGTATCTGAAGT 3780 Dc 3721 ATAATGAGTTGCACAATTAGGTGAGCTGTCTCAAAGTATCTGAAGTTATCTGAAGT 3780 Dc 3721 ATAATGAGTTGCACAAATTAGGTGAGCTGTGTGTCTCAAAGTATCTGAAGT 3780 Dc 3721 ATAATGAGTTGCACAAATTAGGTGAGCTGTGTGTCTCAAAGTATCTGAAGTTATCTGAAGTTACTACTGAAGTTACTGAAGTTACTGAAGTTACTACTGAAGTTACTACTGAAGTTACTACTACTACTACTACTACTACTACTACTACTACTAC	Oy 3781 ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTGAAGTATTTTAGTGACA 3840 Db 3781 ATCTGAACTACTTTATTCTCTCGAATTGTATTACAAACATTTGAAGTATTTTAGTGACA 3840 Qy 3841 TTATGTTCTAACATTGTACTACACATTTGTTACAACATATAGTGACA 3840 Db 3841 TTATGTTCTAACATTGTCAAGATAATTTGTTACAACATATAAGGTACCACTGAAGCAGT 3900 Qy 3801 GACTGAGATTGTCAAGATAATTTGTTACAACATTATAAGTGAAGCAGT 3900 Qy 3901 GACTGAGATTGCCACTGTAGAAAATTTATAACATTTATCATTGAACCTGGA 3960 Db 3901 GACTGAGATTGCCAACTGTAACAACATTTATCATTGAAACCTGGA 3960	ATTGTTGATTATCTTAAAAATGCAAAT 40 ATTGTTGATTATCTTAAAAATGCAAAT 40 TGTACATTAAATGCATATTTCTTGATA 40 TGTACATTAAATGCATATTTCTTGATA 40 TGTACATTAAATGCATATTTCTTGATA 40 AAAGCGGCCCGACAGCAACGG 4134 AAAGCGCCCGACAGCAACGG 4134	RESULT 8 US-10-268-051-7 US-10-268-051-7 Sequence 7, Application US/10268051 Patent No. 6748900 GENERAL INPORMATION: APPLICANT: Harris, H. William APPLICANT: Russell, David R. APPLICANT: Russell, David R. APPLICANT: Betka, Marlies APPLICANT: Marlies APPLICANT: Betka, Marlies APPLICANT: Marlies APPLICANT: Marlies APPLICANT: APPLICANTION NUMBER: US/10/268,051 CURRENT APPLICANTON NUMBER: G0/328,464 PRIOR FILING DATE: 2001-10-11 NUMBER: OF SEQ ID NOS: 13 SOFTWARE: PatentIn version 3.1 SEQ ID NO LENGTH: 4134 TYPE: DNA CRANISM: Squalus acanthias

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1021 GACCAACACCACCACCACCACAACATCATCAACACTTCCAATGAACTCAGGGGGAACTCGGGAACTCGGGGAACTCGGGGAACTCGGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCGGGAACTCACCAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCACCAACTCGAACTCGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCGAACTCAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               561 CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTAAAATCGAGACCGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 CTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGAAAGGAGACATCATACTGGGAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

APPLICATION NUMBER: 08/353,784

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 22 Cotober, 1993

APPLICATION NUMBER: U.S. 08/001,127

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/934,61

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/934,044

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNYAY AGGNT INFORMATION:

REFERENCE/COCKET NUMBER: 213/005

TELERX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

FINNTHH. 3809 base pairs
                                                                              ADDRESSEE: LYON & LYON
STREET: First Interstate World Center
STREET: 633 West Fifth Street
CITY: Los Angeles
STREET: Galifornia
CONNTR: Galifornia
CONNTR: USA
ZIP: 90071
COMPUTER READABLE FORM:
WEDIUM IYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1745.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NSOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 76.4%;
Matches 2187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3809 base pairs
TYPE: nucleic acid
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 373..36
COTHER INFORMATION
US-08-485-588-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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   3181 ATCTCCTCGCCCCCCCTCGTCCACCTGCGGCCGGCCTCACCATGGAGATGCAGCGCTGC 3240
                                                                                                                       3241 AGCACGCAGAAGGTCAGCTTCGGCAGCGGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG
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                                                              3241 AGCACGCAGAAGGTCAGCTTCGGCAGCGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG
                                                                                                                                                                                   ACAGGCGATACGCCACCCTCAGCCGCACGGCCCGCAGGAACTCGGCGGATGGCCGC
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Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Porrest H. Puller
APPLICANT: James E. Garrett, Jr.
IIILE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
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US-08-485-588-3
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1701 CCTGAGGATCTCCTACAATGTATCGAGGCGTCTACTCCATTGCCTCCCCCTGCAGGA 1570 1611 TTTACGATTACTCCAAATGTATCTACCAGTCTACTCACTC	2721 CCATGAGCIGGAGGACGAGCTCATCATCACCTGCGACGAGGCTCGCTCATGGCGCT 2780 [
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Pred. No. 0;
0; Mismatches
                                              APPLICATION NUMBER: PC.1/US/34/1211/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 PEDTUATY, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 21 FEDTUATY, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 23 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 12 AUGUST, 1991
ATTORNEY, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 32 AUGUST, 1991
ATTORNEY, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 33 AUGUST, 1991
ATTORNEY, 1992
ATTORNEY, 1993
ATTORNEY, 1994
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
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Best Local Similarity 76.4%;
Matches 2187; Conservative
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3809 base pairs
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LOCATION: 373..3606
COTHER INFORMATION:
US-08-484-565-3
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   GGGCTTCCTGATCGGCTACACCTGCCTGCTGCTGCCATCTGCTTCTTTGCCTTCAA
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: described below: 9
08/353,784
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5/63569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James B. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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LOSE: Lyon & Lyo
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyor
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STREET:
CITY: Lo
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US-08-484-565-3
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201 CTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCGAGCAGCAGCAGCAGGAAGGG 2120 11971 CTCCAGGGAGGCCCTTTCCAACTGCAGGAAGCCGAGCAGGAAGGG 2120 2111 GATCATCCAGGGGGGGGCCTTCCAACTGCAGGAAGCCTTCGCAGGAAGCACCAGGAAGGG 2120 2112 GATCATCCAGGGGGGGGGCCTTCCAACTGCAGGAAGCACCTGCAGGAAGCAT 2180 2111 GATCATCCAGGGGGGGGGGGGTGCTTTCAACTGCAGGAAGCACCTGCAGGAAGCAT 2180 2111 GATCATCAACACACACCTCTCTTCATCTGTTTCAACTGCTCGAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCATTGCAGGAAGCACCTGCAGGAAGCACCTGTTCAGGAAGCACCTGTTCAGGAAGCATTGCAGGAAGCACCTGTTCAGGAAGCATTGCAGGAAGCACCTGTTCAGGAAGCATTGCAGGAAGCACCTGTTCAGGAAGCACCTGTTCAGGAAGCATTGCAGGAAGCACTGCAGGAAGCATTGCAGGAAGCACCTGTTCAGGAAGCACTGCAGGAAGCACCTGTTCAGGAAGCACTTCAGGAAGCACTGCAGGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCCAAACCCAGAAGCACCAAACCCAGAAGCACCCAAACCCAGAAGCACCAAACCCAGAAGCACCAC	CTCTTCATCGTCGGGAGCTCTTCATTCCAGCCTATGCGCAGCACCTATGGT 287 GTCGGCCGTGGAGGTCATTCCAGCCTATGCCAGCACCTATGGGAGGTTTTGT 287 GTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTTGGGCTGCTGGGCTGCTTTT 302 CTCTGCCGTAGAGGTGATTGCCATCCTGGCAGCCGCCGCTTGGTTGCTTGGCTGCTTTT 293 CTTCAACAAGTTACATCATCATCATCAGCCGTGCCGCAACACACCATCGAGGAGGTGCG 308 CTTCAACAAGATCTACATCATCTTCAAGCCGTGCCGCAACACCCATCGAGGAGGTGCG 299 CTTCAACAAGATCTACATCATCATCAAGCTGCCGCAACACCATCGAGGAGGAGGG 299 CTGCAACAAGATCTACATCAAGATGGCGGCCCGGAGCACCCATCGAGGAGGAGGG 314 CTGCAACAAGATCTACATCAAGATGGCGGCCCGGGCCCCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                    Length 3809;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 1745.2;
Pred. No. 0;
0; Mismatches
TELEFAX: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 bace
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                                                                                                                                                                                                                      CDNA to mRNA
                                                                                                                        LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 2187; Conservative
                                                                                                                                                                                                                                                              ) NAME/KEY: CDS
LOCATION: 373.3606
) OTHER INFORMATION:
US-08-480-751-3
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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       3051 CGTCTCCCGCAAGCGGTCCAGCAGCCTTGGAGGCTCCACGGGATCCACCCCCTCCTCCTC 3110
                                                                                                                             11 CATCAGCAGCAGAAGACCAACA----GCGAAGACCCATTCCCACAGCCCGAGAGGCAGAAG 3165
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                                                                                 CACCTGCGGCCCGGGCCTCACCATGGAGATGCAGCGCTGCAGCACGCAGAAGGTCAGCTT
                                                                                                                                                                                                                                                                        3321 CAGCCGCACGCCCCCAGCAGCACTCGGCGGATGGCCGCAG 3362
                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: 08/35/184
APPLICATION NUMBER: 07/05/94/12117
FILING DATE: 23 Adguer, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/09/389
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/84,044
FILING DATE: 13 Adguer, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 33 Adguer, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08480751
Patent No. 5858684
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Lyon & Lyon
First Interstate World Center
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
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STATE: California
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STREET:
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US-08-480-751-3
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42.2%; Score 1745.2; DB 2; Length 3809;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 658; Indels 17;
APPLICANT: Steven C. Hebert
APPLICANT: Janes E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEOFENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                       OPERATION SYSTEM: PC-DOS/MS-DOS
SOPTWARE: FASTEG
CURRENT APPLICATION DATA:
PAPPLICATION NUMBER: US/08/943,986
FILING DATE: 03-007-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
FILING DATE: 10 October, 1994
APPLICATION NUMBER: US/08/94/12117
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: US. 08/203,897
FILING DATE: 23 AUGUST, 1993
APPLICATION NUMBER: US. 08/009,389
FILING DATE: 22 October, 1993
APPLICATION NUMBER: US. 08/0017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 11 AUGUST, 1992
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 11 February, 1993
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 11 February, 1991
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: US. 07/934,61
FILING DATE: 23 AUGUST, 1991
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ANNA: Leber SALIAND
                                                                                                                                     E: Lyon & Lyon
First Interstate World Center
Suite 4700
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMPUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELEFA: (7-35:0
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleicaid
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                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: FASTSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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OTHER INFORMATION:
US-08-943-986-3
                                                                                                                                                                                                                          Los Angeles
: California
RY: USA
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1082 1220 1280 1202

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CLASSIFICATION: 514

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 8

APPLICATION NUMBER: PCT/US/94/12117

APPLICATION NUMBER: U.S. 08/292, 827

FILING DATE: 22 October, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 Sctober, 1993

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 22 Sebruary, 1993

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 21 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/934,61

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/934,61

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179
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REGISTRATION NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELERA: (7.3510
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 76.4
Matches 2187; Conservative
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; LOCATION: 373..36
; OTHER INFORMATION:
US-08-353-784-3
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Patent No. 6031003
GENERAL INFORMATION
APPLICANT: Edward F. Nemeth, Edward M. APPLICANT: Brown, Steven C. Hebert, APPLICANT: Brown, Steven C. Wan Wagenen, APPLICANT: Brown, Steven C. Wan Wagenen, APPLICANT: Brown, Steven C. Wan Wagenen, APPLICANT: Porrest H. Fuller, Eric G. APPLICANT: Delmar, Scott T. Moe TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE ITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 4 Non & Lyon
STREET: Silter Interstate World Center STREET: Silter ADDRESS STREET: Silter 4000
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb StCOMPUTER: EastSEQ for Windows Version: SOFTWARE: FastSEQ for Windows Version: SOFTWARE: FastSEQ for Windows Version: SOFTWARE: TastSETCATION DATA: Windows Version: Tolk Date: 7 June, 1995
FILING DATE: 7 June, 1995
FILING DATE: 9 December, 1994
APPLICATION NUMBER: 08/353,784
FILING DATE: 21 Actober, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/31,161
FILING DATE: 21 August, 1993
APPLICATION NUMBER: U.S. 08/01,127
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 FORWATION: NAMER: DOUGLAS C. Murdock
REGISTRATION NUMBER: 37,549
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                                                                                                                                                                                                                                                   DB 3; Length 3809;
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                                                                                                                                                                                                                                                                              658;
                                                                                                                                                                                                                                                 42.2%; Score 1745.2; 76.4%; Pred. No. 0; cive 0; Mismatches
REFERENCE/DOCKET NUMBER: 213/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0470
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 3899 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                          CDS
373..3606
                                                                                                                                                linear
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Best Local Similarity
Matches 2187; Conserv
                                                                                                                                                                                       NAME/KEY:

LOCATION:

US-08-484-719B-3
                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDION TYPE: 3.5. DISECTOR, 1.44 FED SCORGES COMPUTER: IBM PC compatible SOFTWARE: PASTED COMPUTER: PASTED COMPUTER: PASTED CORRENT APPLICATION DATA: PCOCEDE 23, 1995
CLASSIFICATION NUMBER: US/08/546,998
FILING DATE: OCCEDE 23, 1995
CLASSIFICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: PRIOR APPLICATION DATA: described below: PRIOR APPLICATION DATA: described below: FILING DATE: MADMER: 125/304
FILING DATE: NUMBER: 215/304
FELERNICE FOCKET NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
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42.2%; Score 1745.2; DB 3;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 658;
APPLICANT: Van Wagenen, Bradford C.
APPLICANT: Moe, Scott T.
APPLICANT: Balandrin, Manuel F.
APPLICANT: Balandrin, Manuel F.
APPLICANT: DelMar, Eric G.
APPLICANT: Nemeth, Edward F.
TITLE OF INVENTION: CAMCINE ECEPTOR-ACTIVE
TITLE OF INVENTION: CAMCINE ECOMPOSES:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Gaile 4700
STREET: Gaile 4700
STREET: Gailfornia
CCUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mb storage
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EDNESS: single
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| LOCATION: 373...3606
| OTHER INFORMATION:
| US-08-546-998-2
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          GCTGCTCCTCCCTCATCTGCTGCTTCTCCAGCTCGCTCATCTTCATCGGCGAGCCCAG 2480
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; Sequence 2, Application US/08546998
; General No. 6211244
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            3081 CIGCAGCACGCCCACGCCTTCAAGGTGGCGGCCCGGGCCACCCTCCGGCGCAGCGC 3140
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 17, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 17, Appl	Seguence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Seguence 23, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 117, App
σι	US-09-975-553-17	US-10-125-792-1	US-10-125-778-1	US-10-270-795-17	US-10-270-876-17	US-10-268-051-7	US-10-125-772-1	US-10-016-496-1	US-10-411-076-23	US-10-410-872-17	US-10-410-885-1	US-10-225-567A-117
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ALIGNMENTS

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Sequence 17, Application US/09975553

Sequence 17, Application US/09975553

Patent No. US20020152968A1

APPLICANT: Harris, H. William, Jr.

APPLICANT: Harris, H. William, Jr.

APPLICANT: Nearing, J. acqueline

APPLICANT: Berka, Marlies

TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

TITLE OF INVENTION: Webber 1004-001

CURRENT FILING DATE: 2000-10-11

PRIOR PRIDK APPLICATION NUMBER: 09/687,477

PRIOR FILING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: 09/687,477

PRIOR FILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

SOFTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 4134

CREAL DATE

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Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps

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12 60/240,003 12 3.1	Cuery Match 100.0%; Score 4134; DB 14; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; Matches 4134, Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AATTCCGTTGCTGTCGGTTCAGTCCAAGTCCTCCTCCAGTGCAAAATGAGAAATGGTGTC 60 Db 1 AATTCCGTTGCTGTCGGTTCAGTCCAAGTCTCCTCCAGTGCAAAATGAGAAAATGGTGGTC 60	QY 61 GCCATTACAGGAACATGCACTACATCTGTGTAAATGAAATATTGTCAGTTATCTGAAGGT 120 Db 61 GCCATTACAGGAACATGCACTCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 QY 121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCATTCTGCACGTTTTCCCATT 180 QY 121 TATTAAAATGTTTCTGCAAGGATGGCTTCACGAGAAATCAATTCTGCACGTTTTCCCATT 180	181 GTCATTGTATCATAACTGACCAAAGGGTTAACAAATGGAACAAAGGGCGCCCCCCCC	Db 241 GTTCACCCTTTCTTGGAGCATACGATCAACCCTGAAGGAGATGGAAGACTTGAGGAGGAA 300 OY 301 ATGGGGATTGATCTTCCAGGAGTTCTGCTGAAAGCGATCCCTCACCATTACAAGATAA 360 Db 301 ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCTCACCATTACAAGATAA 360		481 CTCCTACAGTCGTACAATGCCTCACAATCGCCAAACCAAACGAAAGGAAGAAGGGCCCCAAACGAAGGAAGAA	Db 541 GACATCATACTGGGAGGTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600 Qy 601 TTAAAATCGAGACCGGAGGCGACAAAATGTATTCGGTACAATTTTCGAGGCTTCCGATGG 660 Db 601 TTAAAATCGAGACCGGAGGCGAAAAATGAAAATTTCGGTACAATTTTCGAGGCTTCCGATGG 660 Qy 661 CTCCAGGCGATGATTCGCAATAAAAAAAAAAAAAAAAATTTCCTGCCCAAT 720	Db 661 CTCCAGGCGATGTATTGAGGGATTAACAGGATTTGAGGGTTTTCTGCCCCAAT 720 Qy 721 ATCACCTGGGATATTGGCATATTGACAGGGTAACACCGTGTCCAGGGGGTAAGGCA 780 Db 721 ATCACCTGGGATATTGGATATTGACAGGTAACACCGTGTCCAAGGGGGTTAGGGA 780	OY 781 ACACTCAGCTTTGTGGCCCAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC 840

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APPLICANT: Mearing, Jacqueline A.
APPLICANT: Berker, Marries
TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
FILE REFERENCE: 2213.1006-005
GURRENT APPLICATION NUMBER: US/10/125,778
FRIOR FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 10/121,441
PRIOR APPLICATION NUMBER: 60/240,392
PRIOR PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/240,392
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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100.0%; Score 4134; DB 14; Length 4134;
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Matches 4134; Conservative 0; Mismatches 0; Indels 0;
                                       Sequence 1, Application US/10125778 ; Publication No. US20030082574A1 ; GENERAL INFORMATION:
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OY 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCATTGAAACCTGGA 3960 1	RESULT 4 US-10-270-795-17 US-10-270-795-17 Sequence 17, Application US/10270795 Publication No. US2003008485SA1 Sequence 17, Application US/10270795 Publication No. US2003008485SA1 APPLICANT: Aquablo Product Sciences, LLC APPLICANT: Russall, David R. APPLICANT: Russall, David R. APPLICANT: Nearing, Jacqueline TITLE OF INVENTION: Fish FILE REFERENCE: 2213.2002-000 CURRENT APPLICATION NUMBER: US/09/687,372 PRIOR APPLICATION NUMBER: US/09/687,372 PRIOR APPLICATION NUMBER: US/09/687,372 NUMBER OF SEQ ID NOS: 23 SEQ ID NO 17 LENGTH: 4134 TYPE: DAA TYPE: DAA	Query Match 100.0%; Score 4134; DB 14; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; 0; Indels 0; Gaps 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 AATTCCGTTGCTGTCGAGTCCAAGTCCAAGTCCAAGTCAAAATGAGAAATGGTGGT 60 0; Indels 0; Gaps 0; Oy 61 GCCATTACGTGCTGCGTTCAAGTCCAAGTCTCCCAGTGCAAAATGAGAAATGGTGGT 60 61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTATCTGAAGGT 120 Oy 61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTGTCAGTTTATCTGAAGGT 120 120 Oy 121 TATTAAAATGTTTCTGCAAGGATGGATTCACGAGAAATCAAATTGTCAGTTTACCCATT 180 Oy 121 TATTAAAATGTTTCTGCAAGGATGGATCACACAGAACAAAATGGAACAAAGTTACCCATT 180 Oy 181 GTCATTGTAGAATAACTGACCAAAGGATCAAAAAAAAAA

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100.0%; Score 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 10/121,441
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2001-01
PRIOR PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/240,392
PRIOR APPLICATION NUMBER: 60/240,003
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
SOFWARE: PATENTING DATE: 2000-10-12
SOFWARE: PATENTING DATE: 2000-10-12
SOFWARE: PATENTIN VERSION 3.1
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APPLICANT: Marisal
APPLICANT: Harris, H. William
APPLICANT: Harris, Jacqueline A.
APPLICANT: Betka, Marlies
TITLE OF INVENTION: POLYVALent Cation-Sensing Receptor in Atlantic Salmon
FILE REFERENCE: 2213.1006-006
CURRENT APPLICATION NOWBER: US/10/125,772
     AGCACGCAGAAGGTCAGCTTCGGCAGCGGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG
                  AGCACGCAGAAGGTCAGCTTCGGCAGCGGCACCGTCACCCTGTCGCTCAGCTTCGAGGAG
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US-10-016-496-1
Sequence 1, Application US/10016496
Sequence 1, Application US/10016496
Sequence 1, Application No. US20030166908A1
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
ITILE OF INVENTION: Polycation-Sensing Receptor in Aquatic
ITILE OF INVENTION: Polycation Species and Methods of Use Thereof
ITILE OF INVENTION: Polycation Not 1001.007
CURRENT APPLICATION NUMBER: US/10/106,496
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US/09/162,021B
PRIOR FILING DATE: 1998-09-28
PRIOR FILING DATE: 1998-09-28
PRIOR PILING DATE: 1998-09-28
PRIOR PILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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LOCATION: (43)
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AGCACCTACGGCAAGTTTGTGTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTC 3000
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3301 ACRESCOCRATICACION	RESULT 11 US-10-411-885-1 Sequence 1, Application US/10410885 Fublication No. US2003023466A1 GENERAL INFORMATION: APPLICANT: Harris, H. William APPLICANT: Becka, Marlies TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon FILE REFERENCE: 2213.1006-008 CURRENT APPLICATION NUMBER: US/10/410,885 CURRENT FILING DATE: 2003-04-09 PRIOR FILING DATE: 2003-04-09 PRIOR FILING DATE: 10/125,778 PRIOR PELING DATE: 10/125,772
161 GCATGTGGAGGGAGAATTCAGTGAAAACGAAGTGCAAGTGCGTGTACAAAGTGCCCCCCAAGGAGATCCCCCCCC	3061 AACACCATGAAGAGCTGCAAGACGACCACGCCTTCAAGGTGGCGCCCGG 3120 3161 AACACCATCGAGGAGGTGCCACGCCACGCCACGCTTCAAGGTGGCGCCCGG 3120 3121 GCCACCTCCGGCGCAGCGCGCGTCTCGCAGCCTCTAAGGTGCGGCTCCACC 3180 3121 GCCACCTCCGGCGCGCGCTCTCGCAGCGCTCCAGCAGCTCTGCGGCTCCACC 3180 3121 GCCACCTCCGGCGCGCGCGTCTCGCAGCGCTCCAGCAGCCTCCACC 3180 3181 ATCTCCTCGCCGCCTCCTCCACCGGGCCCGGGCTCACCATGGAGATGCAGCGCTCCACC 3240 [

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 10/125,792
PRIOR PELING DATE: 2002-04-18
PRIOR PELING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2001-10-11
PRIOR PELING DATE: 2001-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
SOFTWARE: PATENTING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VERSION 3.2
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1012 CTATGGCGGCCCAGGCATGACCAGGAGCGGGGGGGGGCCCTAAATGCAGCTGAACTGCTAT 1160 1013 CTATGGCGCCCCAGGCATGACCAGGAGCGGGGGGGGGCGCCCAGGCGGGGGGGG	2121 GATCATGGAGGGGAGCCCACTGCTGCTTTGAATGGATGGCATGTGCAGAGGGAGTT 2180
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4021 TOTRATCHGARGTOTRAAATAGAAAAAAAAAAAAAAAAAAAAAAAAAA	DS 903 GAATCAATTCAAGTCTTTCCTCCGAACCATCCCCAATGAGCACCAGGCCACTGCCAT 962 Qy 1041 GGCCGAGATCATCGAGTGCACTTCCAGTGGGTGGGAACCCTGGCAGCGACGATGA 1100

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2181 CAGTGATGAAAACGATGCAAGTGCGTGTACAAAGTGCCCGAATGATTTCTGGTCGAATGA 2240	OY 3261 CGGCAGCGGCACCGTCACCTTGAGTTGAGGAGACAGGCGGTACGCCTT 3320
GAACCACACGTGGCATGGCCAAGGAGATCGAGTACCTGTCGTGGACGGAGGCCCTTGG 230	Qy 3321 CAGCCGCAGGGCCCGCAGCAGCAGCAGCGGATGGCCGCAG 3362
2301 GATCGGTCTGACCATCTTCGCCGTACTGGGCATCCTGATCACCTCCTTCGTGCTGGGGGT 2360	RESULT 13 US-10-305-720-1432 ; Sequence 1432, Application US/10305720 ; Publication No INSONADOLOGISAN
2361 CTICATCAAGITCAGGAACACTCCCATCGIGAAGGCCACCAACCGGGAGITGITCTACCT 2420 	GENERAL INFORMATION: ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J. ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGTCATCTTCATCGGCGAGCCCAG 2480	CURRENT APPLICATION NUMBER: US/10/305,720 ; CURRENT FILING DATE: 2002-11-26 ; FRIOR APPLICATION NUMBER: 09/016,434
2481 GGACTGGACCTGTCGGCTAACCGGCCTTTGGCATCAGCTTCGTCCTGTGCATCTC 2540	01
2541 CTGCATCCTGGTGAAGACCAACGGGTGCTGGTCTTTGGAGGCCAAGATCCCCACCAG 2600) Therefore 5254) TYPE: DNA) ORCANISM: Homo sapiens) PEATURE:
2601 CCTCCACCGCAAGTGGGTGGGCCTCAACCTGCAGTTCCTCCTGCGTCTTCGCATCCT 2660	; NAME/KEY: misc_feature ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g599819 US-10-305-720-1432
GGTGCAAATGGTCACCTGCATCTACCTCTACCGCCTCCCTC	Query Match 42.2%; Score 1743.6; DB 16; Length 3234; Best Local Similarity 76.4%; Pred. No. 0; Matches 2186; Conservative 0; Mismatches 659; Indels 17; Gaps 3;
CATGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	OY 501 CTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGAAAGAA
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GTCGGCCGTGGATCTCCTTCCAGCCTACCCAGCTGCCAGCTGGCAAGTTGG GTCGGCCGTGGAGGTGATTGCCATCCTGGCCTTCGAGCTTCGGGCTGCTGGGCTGCATTTA 302	OY 741 ATTTGACACGTGTACCGTGTCCAAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800
CTICALCAGAGGIGATISCCATCTIGGCAGCCAGCTIGGCTIGCTGGCGTGCTTT 293 CTICAACAGTGTTACATCGTGTTCAAGCCGTGCCGTAACACCCATCGAGGAGGGGGTGCG 308	OY 801 GAACAAAATCGACTGGAACTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC 860
CITCAACAAGATCIACAITCITCITCAAGCCATCCGCAACACCAICGAGGAGGGGGG 299 CIGCAAGCACGGCGCCACGCCITCAAGGGGGGCCCGGGGCACCCTCCGGGCCACGCC 314	Qy 861 CACAATAGCAGTGGTCGGGGAACCGGGTCGGGAATCTCCACGGCTGTGGCCAATCTATT 920
TIGCAGCACCACAGCTCACGCTITCAAGGTGGCTGCCCGGGCCACGCTGCGCCCCCAAA 305 CGCGTCTCGCAAGCGCTCCAGCAGCTGCGGCTCCACCATCTCCTCGCCCGCC	Oy 921 GGGATTATTTACATTCCACAGGTCAGCTATGCCTCCGAGCAGGCTGCTCAGCACAA 980
3201 CACCTGCGGGCCGGGCCTACCATGGAGATGCAGCGTCACGGGATCCACCCTTCTTCTTCTTCTTCTCTTCTTCTTCTTCTTC	OY 981 GAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGATGAGCAACAGGCCACGGCCAT 1040
3111 CATCAGCAAGAAGAACAGCGAAGACCCATTCCCACAGCCCGAGAGGCAGAAG 3165	1041

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981 GAATGAGTACAAGGCCTTCCTGAGGACCATCCCCAATGATGAGGCAACAGGCCACGGCCAT 1040	1161 TRACTIONAGE AND CONTRICATE AND	1567 CTATGCCAAGAAGGAAAAAGACTCTTCATCAAGAGAAAAATCCTGTGGAGTT 1626
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QY 3261 CGGCAGCGGCACCGTCACCTGTCGCTCAGCTTCGAGGACAGGCCGATACGCCACCT 3320 Db 2794 CAGCAGCAGCTGGCCCTAACCCAGCAGCAGCAGCAGCCCTGACCCTCCCA 2853 QY 3321 CAGCCGCACGGCAGCAGCAGAACTCGGCGGATGGCCGCAG 3362 Db 2854 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGATGCCCGAG 3362 Db 2854 CAGCAGCAACGAATCTCAGCAGCAGCAGAATGCAAGCAGAAG 2895	10-002-184-1 Sequence 1, Application US/10002854 Pubblication No. US2020132224A1 Septimization No. US2020132224A1 APPLICANT: Scadden, David T. APPLICANT: Olszak, Twona T. APPLICAN	OY 921 GGGATTATTATATATCATCAGGGGTATGCCTCCTCGGGGGGGG

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Page 29

	RESULT 15 US-09-727-205-1 i Sequence 1, Application US/09727205 j Patent No. US20020064813A1 j GENERAL INFORMATION: APPLICANT: ELLS, CATHERINE E. TILE OF INVENTION: MONEY CALCIUM SENSING RECEPTOR FILE REPERENCE: QP-70665 CURRENT APPLICATION NUMBER: US/09/727,205 CURRENT APPLICATION NUMBER: GS/06/168,342 PRIOR APPLICATION NUMBER: 60/168,342 PRIOR FILING DATE: 1999-12-01 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 3237 TYPE: DNA COGANISM: MACACA CYNOMOLGUS US-09-727-205-1	Query Match 42.0%; Score 1737.2; DB 9; Length 3237; Best Local Similarity 76.2%; Pred. No. 0; No. 0; Matches 2182; Conservative 0; Mismatches 663; Indels 17; Gaps 3 QY 501 CTCAGGGTATGGTCCAAACCAAAGGGCCCAGAAGGAAGGA	Oy 561 CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTAAAATCGAGGGC 620	QY 681 AATTGAAGAGATTAACAACAGTATGACTTTCCTGCCCAATATCACCCTGCGATATCGCCT 740 Db 231 CATAGAGGAGATAAACAGCAGCCCTTCTTCCCAACTTGACGCTGCGATACAGGAT 290 741 ATTTGACACGTGTAACACCGTGTCCAAGGCGCTAGAGGAACACTCAGGTTTGTGCCCCA 800 Db 291 ATTTGACACCTTGCAACGCGTTCTAAGGCCTTGGAAGCCACCCTGAGTTTTGTTGCTCA 350		411 TACGATTATTATACATTCCACAGGTCAGCTATGCCTCTCCAGGGGGCTGCTCAGCAACATGCTATGCTATGCTTATGCTTAGCAACAAAACATGCTATGCCTCCTCGAGGAGGCTCAGCAACAAAAAAAA
Oy 2061 CTCCAAAGTGGTTCCTTTCTCCAACTGCAGTGTGTGTGCCGGGCACCAGGAAGGG 2120 1627 CTCCAGGAGGTGCCTTTCTCCAACTGCAGCCGAGACTGCTGGCAGGCA	2301 GATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATCACC	Oy 2601 CCTCCACGGAAGTGGGCCTCAACCTGCAGTTCCTCCTGGTCTTCGCATCCT 2660 Db 2167 CTTCCACCGCAAGTGGTGGGGGCTCAACCTGCAGTTCTGCTCTGCACCTT 2226 Oy 2661 GGTGCAAATGGTCACCTGCATCATCTGCTTCACCTCCTCCTCCAGTACAGGAA 2720 Db 2227 CATGCAGAATGGTCATCATGAGCTCTACACGGGCCCTCCCT	Qy 2721 CCATGAGGTGGAGGAGGTCATCTTCATCACCTGCGAGGGGTCGCTCATGGCGCT 2780 Db 2287 CCAGGAGGTGAGGATCATCTTCATCACGAGGGCTCCCTCATGGCCT 2346 Qy 2781 GGGCTTCCTCATCGGCTACCTGCCTCCTCGCCGCCATCTGCTTCTTCTTCGCTTCAA 2840 Db 2347 GGGCTTCCTCGATCGCTACACCTGCCTGCTGCTGCTTCTTCTTTGCCTTCAA 2406	QY 2841 GTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTCATCACCTTCAGCATGTTGAT 2900 Db 2407 GTCCCGGAAGCTGCCGGAGAACTTCAATGAAGCCAAGTTCATCACCTTCAGCATGCTCAT 2466 QY 2901 CTTCTTCATCGTCTTCATGATCTCCCTCGCCGCCTATGTCAGCACCTTTGT 2960 Db 2467 CTTCTTCATCGTCTGATCTCCTTCATTCCAGCCTATGCCAGCACTTTGT 2960 CA 2467 CTTCTTCATCGTCTGATCTCCTTCATTCCAGCCTATGCCAGCACTTTGT 2526	2961 GTCGGCCGTGGAGTGATTGCCATCCTGGCCTCCAGCTTTCGGGCTGCTGTGGCTGCATTTA 2527 CTCTGCCGTAGAGTGATTGCCATCCTGGCAGCTTTGGCTTGCTGGCGTCCTT 3021 CTTCAACAAGTTAACATCATCCTGTTCAAGCGTGCCGTAACACCATCGTGGGGGGGG	CAACAAGACCTACATTCTCTTCAAGCCATCCCGCAACAATCCATCC

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2300 2360 2420 2480 2780 2318 2378 2438 2498 3020 2558 3140 2078 2600 2198 2258 2840 CAGCGATGAGACAGATGCCCAGTGCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGA CETCTCCCGCAAGCGGTCCAGCAGCCTTGGGGGCTCCACTGGATCCACCCCCTCCTC GAACCACACGTCGTGCATCGCCAAGGAGATCGAGTACCTGTCGTGGACGGAGCCTTCGG GCTGCTCTTCTCCCTCATCTGCTTCTCCAGCTCGCTCATCTTCATCGGCGAGCCCAG GGGCTTCCTGATCGGCTACACCTGCCTGCTGCTGCCATCTGCTTCTTTGCCTTCAA GAACCACCTCCTGCATTGCCAAGAGATGAGTTTCTGTCGTGGACAGAGCCCTTTGG Gritarcaagriccscaacacsccarccarcaassccaccaasasccrorccraccr GTCGGCCGTGGAGGTGATTGCCATCCTGGCCTCCAGCTTCGGGGCTGCTGGGGCTGCATTTA cricaacaacarcracarcricrricaaccarccccaacacarccaacacaacaacaacarcca CTGCAGCACGGCCCCACGCCTTCAAGGTGGCGGCCCGGGGCCACCCTCCGGCGCAGCGC Trideadedecededecedecentricaadendecedecedecedecedecedecaa GATCATCGAGGGGGGGCCCCACCTGCTTTGAATGCATGGCATGTGCAGGGGAGGGTT CAGTGATGAAAACGATGCAAGTGCGTGTACAAAGTGCCCGAATGATTTCTGGTCGAATGA GATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATCACCTCCTTCGTGGGGGT GATTGCACTCACCCTCTTTGCCGTGCTGGGCATTTTCCTGACAGCCTTTGTGCTGGGTGT CTICALCAAGITCAAGAACACICCCATCGIGAAGGCCACCAACGGGGAGITGICCTACCI GGACTGGACCTGTCGGCCAACCGGCCTTTGGCATCAGCTTCGTCCTGTGCATCTC CTGCATCCTGGTGAAGACCAACCGGGTGCTGCTGGTCTTCGAGGCCAAGATCCCCACCAG grecarcerdergaaaccaaccercrecrecrecreserrreageccaacarceceae CATGCAGATTGTCATCTGTGTAGTCTGGCTCTACACCGCGCCCCCCTCAAGCTACCGCAA GGGCTTCCTCATCGGCTACACCTGCCTCGTCGCCCATCTGCTTCTTCTTCAA GTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTCATCACCTTCAGCATGTTGAT CTTCTTCATCGTCTGGATCTCCTTCATCCCCGCCTATGTCAGCACCTACGGCAAGTTTGT CTTCAACAAGTGTTACATCATCCTGTTCAAGCCGTGCCGTAACACCCATCGAGGAGGTGCG CCTCCACCGCAAGTGGGTGGGCCTCAACCTGCAGTTCCTCCTGGTCTTCCTCTGCATCCT criccarcecaagidegresescricaaccideagrinerscrissinirectericae 2961 2619 2679 2841 2379 2901 2439 2499 3021 2559 3081 90 de de Sy G 8 8 8 g & g ò 1478 2060 CTCCAAAGTGGTTCCTTTCTCCAACTGCAGTGCGTGCTGCCGGGCACCAGGAAGGG 2120 1880 2000 1598 1399 TATATATACCTGCTTACCTGGGAGAGGGCTCTTCACCAACGGCTCCTGTGCAGACATCAA 1358 crascaccrcccadadadadecrccarcercrirraagdaacrcccararracaacer 1538 CTGGCAGCTCTCCGCAGAGGATGAATCGGTGTTGTTCCATGAGGTGGCACTACAACGC 1821 AAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT GGGTGAGCAGGTTGACGATCAAGGTGACCTCAAGGGGAACTACAACATATCAA GGGGGGGGGGGGGCCTTTGATGAGTGTGGTGACCTGGTGGGGAACTATTCCATCAA CATCCACTCTTGCAAACCCGGCACGGCATCTTTGCAAACGGATCTTGTGCAGATATTAA GAAAGTTGAGGCGTGGCAGGTCCTGAAGCACCTACGGCACCTAAACTTTACCAACAATAT crareccaagaaggagaagacrcrrcarcaagagagagaaarccrgrggggrg 1479 1239 1761 1359 1419 1539 1941 2001 2061 1881

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ALIGNMENTS

RESULT 1

AK029770	
LOCUS	AK029770 3115 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male testis cDNA. RIKEN full-length enriched
	library, clone:4930542118 product:calcium-sensing receptor, full
	insert sequence.
ACCESSION	AK029770 -
VERSION	AK029770.1 GI:26325707
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	musculus
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	0
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
	prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	m
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
	Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
	Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
	Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system384-format
	sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the
TITLE	Functional annotation of a full-length mouse CDNA Collection
JOURNAL	Nature 409, 685-690 (2001)
KEFEKENCE	44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
AUTHORS	The Fanium consorcium and the Kinen denome Exploration research

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AUTHORS JOURNAL REFERENCE

TITLE

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AACTGCTACTTCACCGAGAAGACCCTGACGCAGCTGAAGAATTCCAAGGTGCCCTCGCAC 1578
                  1339 GAGGCTTGGGCCAGCTCTTCGCTCATTGCCAAGCCAGAGTACTTCCACGTGGTCGGCGGC
                                                                                                                                                                                          ACCATCGGCTTCGCTCTCAGGGCGGGGGGTATCCCAGGGTTCAACAAGTTCCTGAAGGAG
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PPSSYRNHELEDBIITITCHGGSLMALGSLIGYTCLLAAICFFRNGIYUTT
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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<1. .2352
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 565-573 (2002)
6 (bases 1 to 3115)
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RIKEN.
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(MGD|MGI:1351351, GB|NM_013803, evidence: BLASTN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.3%; Score 1171.4; DB 3; Length 3115; Best Local Similarity 77.1%; Pred. No. 3e-251; Matches 1456; Conservative 0; Mismatches 421; Indels 12;
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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FEATURES

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1938 2058 2118 2178 2238 2298 2418 588 648 768 888 948 <u> AACTGGCAGCTCTCCGCAGAGGATCGATCGGTGTTGTTCCATGAGGTGGGCAACTACAAC</u> GGGATCATCGAGGGGGGGCCCACCTGCTTTGAATGCATGGCATGTGCAGGGGAGAG GAGAACCACACGTCGTGCATCGCCAAGGAGATCGAGTACCTGTCGTGGACGGAGCCCTTC GGAATCGCTCTCTCTTTGCGGTGCTGGGCATTTTCCTGACCGCCTTTGTGCTGGGC ATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAGGGGAACTACACCATTATC 529 Ardecedacededreaccriceardagesedereacciderecedadeacraciacrecarcare 589 AACTGGCACCTCCCCAGAGGACGCTCCATTGTGTTCAAGGAAGTTGGGTACTACAAT GCCTACGCTAAGCCCAGTGACCGACTCAACATCAACGAAAAGAAAATCCTCTGGAGTGGC GTGTATGCCAAGAAGGGAGAAAGACTGTTCATCAATGAGGGGAAGATCTTGTGGAGTGGG TTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCGAGACTGTGTGCCGGGCACCAGGAAG 769 escarcarroacedadadecedacerecrierriricacierericaciereretecendaecedeceae TTCAGTGATGAAAACGATGCAAGTGCGTGTACAAAGTGCCCGAATGATTTCTGGTCGAAT 829 TACAGTGGTGAGACAGATGCGAGTGCCTGTGACAAGTGCCCGGATGACTTCTGGTCCAAT 889 GAGAACCACACTTCCTGCATTGCCAAGGAGATTGAGTTCCTGGCGTGGACTGAGCCCTTT GGGATCGCTCTGACCATCTTCGCCGTACTGGGCATCCTGATCACCTTCGTGCTGGGGG 1009 Grerrearcaagricegaaacaegecearrereaaggeeaceaeegaggaggeereree

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                                       Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TiGR, 9712 Medical Center
Rockville, MD 20850, USA
Tel: 301-388-0200
Fax: 301-388-020
Email: ekirknes@tigr.org
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13.3%; Score 548; DB 9; Length 74
Best Local Similarity 84.8%; Pred. No. 1.3e-111;
Matches 614; Conservative 0; Mismatches 110; Indels
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                                                                                                                                Class: shotgun.

Location/Qualifiers

1. 745

Organism="Canis familiaris"

mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone lib="Dog Library"

/note="Site_1: BstXI; Libraries wer

peripheral blood"
Science 301 (5641), 1898-1903 (2003)
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CE057024.1 GI:35104959
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CICCTGCICTTCICACTCCTCTGCTGCTTCTCCAGCTCCCTGTTCTTCATTGGGGAGCCC 1128
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Canis familiaris

Canis familiaris

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Crania, Canidae, Canis.

1 (bases 1 to 745)

1 (bases 1 to 745)

Rixheses, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                               TCCTGCATCCTGGTGAAGACCAACCGGGTGCTGCTGGTCTTCGAGGCCAAGATCCCCACC
                                                                                                                                                                                                                                                                                    CGCTGCAGCACGGCCCACGCCTTCAAGGTGGCGGCCCGGGCCCACCTCCGGCGCAGC
                                                            CAGGACTGGACCTGCCGCCTGCGACAGCCCGCCTTCGGCATCAGCTTCGTGCTTTGTATC
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Contact: Kirkness BF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Canis familiaris
Canis familiaris
Canis familiaris
Canis familiaris
Canis familiaris
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 637)
1 (kases, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
541 CTGCATCCTGGTGAAGACCAACCGGGTGCTGCTGGTCTTCGAGGCCAAGATCCCCAAG
                                            382 ATGCATCCTGGTGAAAACCAACCGTGTCTCTGGTGTTTGAGGCCAAGATCCCCACAAG
                                                                                                                                                                                                                                                                                                                                                          562 CCATGAGCTGGAGGACGAGATCATCTTCATCACATGCCACGAGGGCTCCCTGATGGCCT
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/organism="Canis familiaris"

/mol type="genoic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: Bstx1; Libraries were prepared from peripheral blood"
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12.0%; Score 495.4; DB 9;
Best Local Similarity 87.1%; Pred. No. 7.6e-100;
Matches 555; Conservative 0; Mismatches 81;
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE303215.1 GI:36094287
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The Institute for Genomic Research
Department of Euraryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Tel: 388-0208
Email: ekirknes@tigr.org
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Canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 746)
1 (karhess, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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/organism="Canis familiaris"
/organism="Canis familiaris"
/organism="Canis familiaris"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site l: BstXI; Libraries were prepared from peripheral blood"
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84.6%; Pred. No. 8.5e-109;
tive 0; Mismatches 111;
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Best Local Similarity 84.6 Matches 613; Conservative
                         CTTC 2904
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

En (Jases 1 to 579)
En (Jases 1 to 579)
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Contact: Fu GK
Contact: Fu GK
Contact: Fu GK
They genomics, Inc.

Incyte Genomics, Inc.

Incyte Genomics, Inc.

Incorporation of partial genes
Contact: Fu GK
Contact: Fu GK
Contact: Fu GK
Incyte Genomics, Inc.

Incyte Genomics, Inc.

Incorporation of partial genes
Incyte Contact: Fu GK
Incyte Genomics, Inc.

Incorporation of partial genes
Incyte Genomics, Inc.

Incorporation of partial genes
Email: gfu@incyte.com
Incorporation of partial genes
Email: gfu@incyte.com
Incorporation of partial genes
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                          Score 452.2; DB 6;
Pred. No. 3.6e-90;
0; Mismatches 73;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 581)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput Gentensian cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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JIGO PORTER DY., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfuedincyte.com.
Location/Qualifiers

1. .581
/ mol_type="mRNA"
/ db_xref="reaxon:9606"
/ clone lib="FLP"
/ note="Vector: pDrive Cloning Vector"
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 600)

Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. 670
| /organism="Canis familiaris"
| /mol type="genomic DNA"
| strain="Standard Poodle"
| /db xref="taxon:9615"
| /clone lib="Cool Library"
| /note="Site 1: BstXI; Libraries were prepared from peripheral Dlood"
                                                                                                                                                                                                                                                                                                                                                    2194 GATGCAAGTGCGTGTACAAAGTGCCCGAATGATTTCTGGTCGAATGAGAACCACACGTCG
                                                                                                                                                                                                                                                                                                                                                                                         574 GATGCAAGTGCCTGTGACAAGTGCCCCGATGACTTCTGGTCCAATGAAAACCACACTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 ATCTGTGTGTGATCTGGCTCTACACGCGCCTCCCTCCAGCTACCGCAACCATGAGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                               TGCATCGCCAAGGAGATCGAGTACCTGTCGTGGACGGAGCCCTTCGGGATCGCTCTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2434 CTCATCTGCTGCTTCTCCAGCTCGCTCATCTTCATCGGCGAGCCCAGGGACTGGACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AAAACCAACGIGICCTCCTGGIGTTTGAGGCCAAGATCCCCACAAGCTTCCACGCAAG
                                                                                                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                     Score 431.6; DB 9; Length
Pred. No. 1.6e-85;
0; Mismatches 89; Indels
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Best Local Similarity 84.5%;
Matches 485; Conservative (
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CD608327/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2647 TTCCTCTGCATCCTGGTGCAAATCGTCACTGCATCATCTGGGTCTAACACGGGGGGTCTCCC 2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2827 TICTICGCCTICAAGTCCCGTAAGCTGCCGGAGAACTICAACGAGGCTAAGTTCATCACC 2886
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
                                                                                                                                                                            519
                                                                                                                                                                                                                                                       459
                                                                                                                                                                                                                                                                                                                                                                                             398 AAGATCCCCACCAGCTTCCACCGCAAGTGGTGGGGGGCTCAACCTGCAGTTCCTGCTGGTT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                458 GTGCTCTGCATCTCATGCATCCTGGTGAAAACCAACGGTGTCCTCGTGGTGTTTGAGGCC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 GAGCTCTCCTACCTCCTCTTCTCCCTGCTCTGCTGCTTCTCCAGCTACCTGTTCTTC
                                                                                                                                                                                                                2467 ATCGGCGAGCCCAGGGACTGGACCTGTCGGCTCCGCCAACCGGCCTTTGGCATCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                       2897 AAGATCCCCACCAGCCTCCACCGCAAGTGGGTGGGCCTCAACCTGCAGTTCCTCCTGGTC
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                                                                                                                                       518 Arcescadececadeacrasacerececrececeaceaceaceacerrasearraseare
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                                                                                                   ۲;
                                                          Length 579;
                                                                                               73; Indels
  /note="Vector: pDrive Cloning Vector"
                                                        Score 440.2; DB 6;
Pred. No. 1.8e-87;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2947 TACGGCAAGTITGTGTCGGCCGTGGAGGT 2975
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GSS.
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                                                          Query Match
Best Local Similarity 87.0%;
Matches 495; Conservative
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CE504040/c
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REFERENCE

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```
EST 12-JAN-2004
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Pu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. 654
/organism="Homo sapiens"
/db type="mRNA"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1819 AAAAAAGTTGAGGCCTGGCAGGTCCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGTGAGCTGACCTTTGACGATCAAGGTGACCTCAAGGGGAACTACACTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTGGCACCTCTCCCCAGAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAAC
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Pred. No. 7.4e-82;
0; Mismatches 128;
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ilarity 79.6%;
Conservative
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CD608329
CD608329.1 GI:4
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Best Local Similarity
Matches 503; Conserv
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
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                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone_llb="FLP"
/note="Vector: pDrive_Cloning_Vector"
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Pred. No. 5.9e-82;
0; Mismatches 104;
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               extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
Email: glugincyte.com.
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Matches 478; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Dases 1 to 602)

Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes

L Genomics 84 (1), 205-210 (2004)

Contact: Pu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.
                                           EST 12-JAN-2004
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                                         CD608328 6021515J1 FLP Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1...602

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/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%; Score 393.2; DB 6;
82.0%; Pred. No. 6.2e-77;
tive 0; Mismatches 103;
                                                                                                     CD608328.1 GI:40256591
                                                                                                                                               sapiens (human)
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Matches 477; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTATGCCAAGAAGGGAGAAAGACTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGG 247
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                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases, 1to 622)

Fu. G. Wang, J. T. Yang, J., Au-Young, J. and Stuve, L.L.

Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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Pred. No. 4e-79;
0; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                   Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tal: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens'
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                   Homo sapiens (human)
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Best Local Similarity 79.4
Matches 489; Conservative
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2273 AGTACCTGTCGTGGACGGAGCCCTTCGGGATCGCTCTGACCATCTTCGCCGTACTGGGCA 2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="mouse (C57BL/6) pancreatic islet library with recombination-based method"
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                                                                                                                                                                                                                                                                       433 AATGTGTTGACTGCCCCGACGGGGATACAGTGATGAGACAGATGCCAGTGCCTGTGAGA
TGTTCCATGAGGTGGGCAACTACAACGCCTACGCTAAGCCCAGTGACCGACTCAACATCA
                         TGTTCGAGGAGGTGGGGTACTACAACGTCTATGCCAAGGTGGCGAGCGGCTCTTCATCA
                                                                              ACGABABABABATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTC
                                                                                                       313 ACGAAAGCAAAATCCTGTGGAGAGGCTTCTCCCGAGTGGTCCCAATTTCCAACTGCAGTC
                                                                                                                                                         2093 GAGACTGTGTGCCGGGCACCAGGAAGGGGATCATCGAGGGGGAGCCCACCTGCTGTTG
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                                                                                                                                                                                                                                   2153 AATGCATGGCATGTGCAGAGGGAGAGTTCAGTGAAAACGATGCAAGTGCGTGTACAA
                                                                                                                                                                                                                                                                                                                   2213 AGIGCCCGAAIGAIITCIGGICGAAIGAGAACCACACGICGIGCAICGCCAAGGAGAICG
                                                                                                                                                                                                                                                                                                                                           Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Ksunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2333 TCCTGATCACCTCCTTCGTGCTGGGGGTCTTCATCAACAGTTCAGGAACAC 2381
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8.1%; Score 336.4; DB 5;
Best Local Similarity 76.6%; Pred. No. 3.3e-64;
Matches 412; Conservative 0; Mismatches 126;
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/dev_stage="adult"
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/clone="mid09082"
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Location/Qualifiers
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/strain="C57BL/6"
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                                                      CK805060 813 bp mRNA linear EST 26-FEB-2004 AGENCOURT 19147865 NICHD XGC Te2 Xenopus laevis cDNA clone IMAGE:721Î077 5', mRNA sequence.
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                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 813)

11 'MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                 Contact: Daniels S. Gerhard, Ph.D.
Contact: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0Ao7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Igor B. Dawid
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMISIOI row: c column: 11
High quality sequence start: 9
High quality sequence stop: 695.
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.larity 73.0%; Pred. No. 1.8e-71;
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                                                                                                                                                                                 Xenopus laevis (African clawed frog)
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AGENCOURT 17636458 NIH MGC_235 Rattus norvegicus cDNA clone
IMAGE:7109300 5', mRNA sequence.
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S NHF-MGC thtp://mgc.nci.nih.gov/.

NHF-MGC thtp://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999).

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genemics

National Cancer Institute / NIH

Bldg. 31 RM10AD/N Bethesda, MD 20892

Email: Gapabs-remail.nih.gov

CDNA Library Preparation: Express Genomics

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clore distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLMA19974 row: j column: 18

High quality sequence stop: 590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2207 GTACAAAGTGCCCGAATGATTTCTGGTCGAATGAGAACCACACGTCGTGCATCGCCAA 2264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567
                                                                                                90 GGCTTTTCACCAACGGGTCCTGTGCAGACATCAAGAAGGTTGAGGCCTGGCAGGTCCTGA
                                                                                                                                                             450 GITITIGAGIGIGAGIGICCIGACGCGAGIACAGIGGIGAGACAGAIGCGAGIGCCI
                                                                                                                                        1847 ACCATCTGCTGCATCTGAAGTTTACCAACAGCATGGGTGAGCTGACTTTGACGATC
                                                                                                                                                                                                           1907 AAGGTGACCTCAAGGGGAACTACACCATTATCAACTGGCAGCTCCCCCAGAGGATGAAT
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                                 30 radocercracicarrececacecerecasanararacacerecracecesases
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Rattus norvegicus
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1727
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LOCUS
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/db_xref="taxon:10116"
/clone="INAGE:1109300"
/tissue_type="kidney, pooled"
/lab host="DH10B TOTA"
/lab host="DH10B TOTA"
/clone lib="NIH MGC_235"
/note="Organ: Kidney; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen before RNA extraction and purification
(Tri-reagent method). CDNA was primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGCGAGCGCGCC(T)25-3' and
cloned into the EcoRV/Not1 sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert size
of 2.2 kb This primary library is non-normalized
(normalized primary library is NIH_MGC_236) and was
constructed by Express Genomics (Frederick, MD). Note:
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Pred. No. 1.1e-62;
0; Mismatches 232;
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us-10-016-496-1.rst

GCTACTCCTTTGGCATGCCCCACAGATAATACCCCTGCTACCGGAAGAGGCC 756

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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
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/lab_host="SOLR"
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/note="Site 1: Xho!" Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
                              BB615658 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4930542118 5', mRNA sequence.

BB615658 GI:16455904
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnas; Lto 633;
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Rikeba, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/clone="4930542118"
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Mus musculus
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                            RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [6] of primer [6] of primer [7] of primer [8] of primer and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the gaptient adapter of sequence [5] of primer adapter of sequence [5] of primer adapter of sequence [7] of primer adapter of sequence [8] of primer adapter of sequence [9] of primer adapter of primer adapter of sequence [9] of primer adapter of p
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US-10-016-496-2 5410 1 MAQLHCQLLFLGFTLLQSYN.......KGTLESPGGSKERPTTMEET 1027 Title: Perfect score: Sequence:

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2002273 segs, 358729299 residues Searched: Total number of hits satisfying chosen parameters:

2002273

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneedp1980s:* geneedp1990s:* geneedp2000s:* geneedp2001s:* geneedp2001s:* geneedp2003ss:* geneedp2003ss:* A_Geneseq_23Sep04:* 1: geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aau76004 Shark kid	Abb78761 Dogfish s	Adhl0917 Shark pol	Abw02706 Dogfish s	Adil9970 Dogfish s	Aaw32059 Dogfish s	Aau00508 Chicken c	Aau02195 Cynomolgo	Aay70325 Human wil	Add48571 Human Pro	Ade62143 Human Pro	Ade62147 Human Pro	Adhl0955 Human par	Adj68365 Human hea	Adi41014 Human GPC	Adi40962 Human GPC	Ado29211 Human GPC	Adj93192 Human ext	Abg72193 Human cal	Aaw11889 Parathyro	Aaw54846 Human par	Aaw38274 Human par	Aay28840 Human cal	Aay41780 Human par	Aaw89565 Human par
QI QI	AAU76004	ABB78761	ADH10917	ABW02706	ADI19970	AAW32059	AAU00508	AAU02195	AAY70325	ADD48571	ADE62143	ADE62147	ADH10955	ADJ68365	ADI41014	ADI40962	AD029211	ADJ93192	ABG72193	AAW11889	AAW54846	AAW38274	AAY28840	AAY41780	AAW89565
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* Query Match	100.0	100.0	100.0	100.0	100.0	97.1	75.9	75.0	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.7	74.7	74.6	4.	74.6	٠	74.6	74.6
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Aay51827 Human cal	Aab74391 Protein e	Aab47822 HuCaR4.0.	Abp81817 Human cal	Aaw11888 Parathyro	Aaw54845 Human par	Aay41779 Human par	Aaw89564 Human par	Aay51826 Human cal	Aab74390 Protein e	Aab47821 HuPCaR5.2	Adm47114 Human cal	Add48589 Human Pro	Aaw38273 Human par	Aaw54844 Bovine pa	Aaw38272 Bovine pa	Aay41778 Bovine pa	Aaw89563 Bovine pa	Aay51825 Bovine ca	Aab47820 BoPCaR1.
AAY51827	AAB74391	AAB47822	ABP81817	AAW11888	AAW54845	AAY41779	AAW89564	AAY51826	AAB74390	AAB47821.	ADM47114	ADD48589	AAW38273	AAW54844	AAW38272	AAY41778	AAW89563	AAY51825	AAB47820
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4037.5	4037.5	4037.5	4037.5	4029.5	4029.5	4029.5	4029.5	4029.5	4029.5	4029.5	4029.5	4029.5	4022.5	3999.5	3999.5	3999.5	3999.5	3999.5	3999.5
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ALIGNMENTS

RESULT 1

Shark kidney calcium receptor related protein-1; SKCaR-RP-1; polyvalent cation-sensing receptor protein; PVCR; fish; flounder; salinity tolerance; fat content; protein content; weight; fish maturation; fish development; spiny dogfish. Shark kidney calcium receptor related protein-1 (SKCaR-RP-1). AAU76004 standard; protein; 1027 AA (BGHM) BRIGHAM & WOMENS HOSPITAL. Hebert SC; 96US-00622738. 97WO-US005031. 98US-00162021 (first entry) (revised) Harris HW, Brown EM, WPI; 2002-163246/21. N-PSDB; ABK14910. Squalus acanthias. 28-SEP-1998; 27-MAR-1996; 27-MAR-1997; 07-AUG-2003 08-MAY-2002 US6337391-B1 38-JAN-2002. AAU76004; PAU76004

New nucleic acid molecule encoding polyvalent cation-sensing receptor protein, useful for regulating adaptation of fish e.g. flounder to marine and fresh water environments, and to alter tissue or meat/muscle composition.

Claim 4; Fig 5A-E; 83pp; English.

polyvalent cation-sensing receptor protein (PVCR), especially Shark Kidney calcium receptor related protein-I (SKCaR-RP-I) that allows fish to sense ion concentrations. The aquatic PVCR allows the successful adaptation of fish, such as flounder, to marine and fresh water environments, and controls maturation and developmental stages in marine species. Modulating the expression of PVCR activates or inhibits PVCR The invention describes an isolated nucleic acid sequence (1) encoding a

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mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. Activating PVCR in epithelial cells increases or decreases salinity tolerance in aquatic species. Regulating salinity tolerance is useful to develop new species of marine fish that are easily adaptable to fresh water aqua culture. The methods are useful for altering body composition e.g. fat content, protein content, weight, thickness, moisture and taster. The species can be maintained in both environments, consecutively to reduce parasites, bacteria and contaminants. This is the amino acid sequence of the shark kidney calcium receptor related protein-1 (SKGR-RP-1), described in the method of the invention. (Updated on 07-AUG-2003 to correct OS field.)
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adult anadromous fish maintained in fresh water prior to transfer to
seawater. The method involves: (a) adding at least one polyvalent cation
sensing receptor (PVCR) modulator to the fresh water; and (b) adding a
feed containing an agent that increases the level of PVCR modulator in
the serum of fish. The PVCR modulator has anabolic activity. The method
can be used for improving the raising of pre-adult anadromous fish e.g.
salmon, char and trout, maintained in fresh water prior to transfer to
seawater. The present sequence represents dogfish shark kidney cation
receptor (SKCaR), which is relative to the PVCRs from salmon, char and
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12-OCT-2000; 2000US-00687476.
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The invention comprises the amino acid and coding sequences of polyvalent cation sensing receptor (PVCR) proteins from Atlantic salmon. The DNA and protein sequences of the invention are useful in the commercial raising of Atlantic salmon and the restoration of wild Atlantic salmon populations, especially in the transfer from freshwater to seawater with increased growth and reduced mortality. The present amino acid sequence represents a shark PVCR-related protein.
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0; Mismatches
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Best Local Similarity 100.0%;
Matches 1027; Conservative 0;
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18-APR-2002; 2002US-00125772.
18-APR-2002; 2002US-00125778.
18-APR-2002; 2002US-00125792.
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Hebert SC;

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The invention relates to aquatic polyvalent cation-sensing receptor (PVCR) proteins and methods of regulating PVCR functions in aquatic species. PVCR is used to screen candidate compounds that may be used to assist fish in adapting to changing ion concentrations by altering water intake, water absorption or urine output and/or for modulating the percentage of total fat, protein and moisture of muscle of the fish. The present sequence is dogfish shark kidney calcium receptor related protein method of the invention
                                                                                                                                                                                                                        Fish polyvalent cation-sensing receptor proteins, useful for assisting fish in adapting to changing ion concentrations by altering water intake and absorption, urine output or for modulating the fat, protein and moisture content of muscle.
                                                                                                                                                                                                                                                                                          Claim 7; SEQ ID NO 2; Opp; English.
                                                                                                                               (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                             27-WAR-1996; 96US-00622738.
27-WAR-1997; 97WO-US005031.
28-SEP-1998; 96US-00162021.
17-NOV-2000; 2000US-00715538.
                                       10-DEC-2001; 2001US-00016496
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N-PSDB; AAD64738.
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MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG 540

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Dogfish shark kidney calcium receptor related protein-I (SKCaR-RP-I).

(first entry)

11-MAR-2004

standard; protein; 1027 AA

ABW02706 ABW02706 Polyvalent cation-sensing receptor; PVCR; anabolic; homeostatic; shark kidney calcium receptor related protein-I; SKCaR-RP-I; dogfish shark; SKCaR-I.

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The present invention relates to methods for improving the raising of pre-adult anadromous fish or preparaing these fish for transfer to seawater by modulating expression of a receptor referred to as the Polyvalent Cation Sensing Receptor (PVCR). The invention is useful in increasing survival and growth and reduce stress of the fish that have been transferred to seawater. The present sequence is a dogfish shark cation receptor (SKCaR) protein.
pre-adult anadromous fish in freshwater comprises adding feed ng an amount of NaCl for fish consumption to the freshwater to the level of the Polyvalent Cation Sensing Receptor modulator the fish.
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stress; dogfish shark; receptor.
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12-OCT-2001; 2001US-00975553.
11-OCT-2001; 2001WO-US031562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein comprises dogfish shark kidney calcium receptor related protein (SKCaR-RP), an aquatic polyvalent cation-sensing receptor (PVCR). Its amino acid sequence was deduced from a kidney cDNA clone (see AAR89290). It shows 74% homology to rat kidney PCVR and bovine parathyroid PVCR and possesses general features that are homologous to PVCR proteins, including a large extracellular domain, 7 transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity tolerance of fish for
                                                                                                            AASRKRSSSLCGSTISSPASSTCGPGLTMEMQRCSTQKVSFGSGTVTLSLSFEETGRYAT
                        LGFLIGYTCLLAAICFFFAFKSRKLPBNFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF
                                                                                         AASRKRSSSLCGSTISSPASSTCGPGLTMEMQRCSTQKVSFGSGTVTLSLSFEETGRYAT
                                                 VSAVEVIAILASS FGLLGCIY FNKCY I ILFK PCRNTI EEVRCSTAAHAFKVAARATLRRS
                                                                  841 VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS
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/note= "region in extracellular domain that is highly
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "region in C-terminal domain that is highly divergent from mammalian PVCR"
                                                                                                                                                                                                                                                                                                                          Calcium receptor related protein; CaR-RP; dogfish shark; SKCaR-RP; polycation-sensing receptor; aquaculture; fish farming; salinity tolerance.
                                                                                                                                                                                                                                                                                                        Dogfish shark kidney calcium receptor related protein (SKCaR-RP)
                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian PVCR
                                                                                                                                                                                                                                             AAW32059 standard; protein; 1026 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 5A-B; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     divergent from
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                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                        PTTMEET 1027
                                                                                                                                                                                           PTTMEET 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-489640/45.
N-PSDB; AAT89290.
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                                                                                                                                                                                                                                                                                                                                                                   Squalus acanthias.
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domains and a cytoplasmic C-terminal domain. Also claimed are: an isolated PVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distallubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for the aquatic PVCR activates or inhibits aquatic PVCR mecivates or inhibits aquatic PVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of marine fish that are easily adaptable to
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5251.5;
Pred. No. 0;
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Best Local Similarity 97.2%;
Matches 1006; Conservative
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The present sequence representing an avian (chicken) calcium-sensing receptor (CaR) is isolated from chicken parathyroid gland cDNA clone CLD. CaR is involved in regulating extracellular calcium homeostasis by controlling PTH (parathyroid hormone) secretion. The polymucleotide encoding car is useful for producing calcium-sensing receptor protein, which can be used to regulate extracellular calcium homeostasis and to regulate serum calcium more rapid growth is obtained due to an increased rate of bone deposition, and eggs of higher quality are increased rate of bone deposition, and eggs of higher quality are corduced. A DNA construct comprising the CAR polymucleotide is useful for developing transgenic animals expressing a mutated form of the calcium-sensing receptor. The CAR polymessing a mutated form of the calcium-sensing receptor. The CAR polymessing a mutated form of the calcium-sensing receptor. The CAR polypeptide can be used to produce antibodies to CAR, which can be used to detect the presence of CAR protein using immunoassays. Also described are methods and compositions which can be used to modulate the serum concentration of calcium in humans and animals
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                                                                                                                                                                                                                                                  Query Match 75.9%; Score 4106.5; DB 4; Best Local Similarity 76.4%; Pred. No. 0; Matches 788; Conservative 85; Mismatches 130;
                                                                                                                                                                                                                              Sequence 1059 AA
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           CDEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .611
/label= Extracellular domain
/note= "Amino-terminal predominantly hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New avian calcium-sensing receptor polymucleotide and encoded receptor protein, useful for regulating serum concentration of calcium animals, particularly in chickens.
                                                                                         ARATLERSAASEKRSSSLCGSTISSPASSTCGPGLTMEMQRCSTQKVSFGSGTVTLSLSF
                                                                                                          EETGRYATLSRTARSRNSADGRSGDDLPSRHHDQGPPQKCEPQPANDARYKAAPTKGTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136..165
/note= "Hydrophobic region characteristic of calcium-sensing receptors and metabotropic glutamate receptor 612..861
/note= "Hydrophobic core comprising helical transmemb
                                                                                                                                                                                                                                                                                                                                                                                                         Avian; chicken; calcium-sensing receptor; CaR; clone ClD; extracellular calcium homeostasis; parathyroid hormone; PTH; serum calcium regulator; bone deposition.
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862. .1059
/note= "Carboxy-terminal hydrophilic domain"
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                                                                                                                                                                                                                                                                                                    standard; protein; 1059
                                                                                                                                                                                                       SPGGSKERPITMEET 1027
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/label= Ma
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/label=
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N-PSDB; AAS01709.
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                                                                                                                                                                                                                                                                                                                                                                                  Monkey; calcium-sensing receptor; bacteria; fungus; protozoa; viral; infection; HIV-1; HIV-2; human immunodeficiency virus; pain; cancer; diabetes; obesity; anorexia; bulimia; Parkinson's disease; stroke; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic; neurological disorder; anxiety; schizophrenia; manic depression; depression; depression; delixium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; vaccine.
              LGFLIGYTCLLAAICFFFFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTYGKF
                                              VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS
                                                           NVSRKRSNSLGGGSTGSTPSSSISSKSNHEDPFPLPASAERQRQQRGCKQKVSFGSGTVT
LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF
                                                                                              AASRKRSSSLCGSTISSPASSTCGPG-------LIMEMQRCSTQKVSFGSGTVT
                                                                                                                                                                                                                                                                                                                                                            Cynomolgous monkey calcium-sensing receptor.
                                                                                                                                                                                                                                                                                   AAU02195 standard; protein; 1078 AA
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BEECHAM PLC.
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N-PSDB; AAS06331.
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heart failure, hypotension, hypertension, urinary retention, osteoporosis, andina pectoris, wycardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delairium, demantia and severe mental retardation, and dyskinesias, such as Huntington's disease or Gilles d'a Tourette's syndrome. The polypeptide is useful for structure-based design of agonist, antagonist or inhibitor of the calcium-sensing receptor. The DNA sequence is useful for chromosome localisation studithe polypeptide and nucleic acid are also useful as vaccines
                                                                                                                                                                                                                                                                                                                                                                   1 MAQIHCQILFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE
                                                                                                                                                                                                                                                                                                     61 ATKCIRYNFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA
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Best Local Similarity 74.3*
Matches 785; Conservative
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Novel Cynomolgous Monkey Calcium-Sensing Receptor polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, asthma, schizophrenia, hypertension, urinary retention, Parkinson's disease and

The sequence represents the amino acid sequence of Cynomolgous monkey calcium-sensing receptor. The calcium-sensing receptor nucleic acid and polypeptide are useful for treating bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancer, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute

Claim 2; Page 28; 38pp; English.

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236 300 296 360 356 420 412

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Q-----RCSTOKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH 984
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                                   ATKCIRYNFRGFRWLQAMIFAIBEINNSMTFLPNITLGYRIFDTCNTVSKALBATLSFVA
                                                              SUBCIRYNFRGFRWLQAMIFAIEEINSSPALLPWLTLGYRIFDTCNTVSKALEATLSFVA
                                                                                                                    QNKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN
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                                                                                                                                                                                                                  IDFSEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS
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MAFYSCCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE
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                                                                                                                                                                                  The present amino acid sequence is the wild type human calcium sensing receptor CaSR, expressed in the kidney. There are multiple alternatively spliced isoforms of CaSR, that arise from partial deletion of residues from this wild type sequence. The CaSR isoforms have hypotensive and osteopathic activity. The isoforms can be used to identify agonists and antagonists that modulate the receptor activity and calcium levels. These modulators are useful for treating hyperparathyroidism or osteoporosis, Pager's disease, hypercalcaemia malignancy or hypercension. The DNA sequence is also useful for altering the CaSR activity and in gene
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      VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIBEVRCSTAAHAFKVAARATLRRS
                           VSAVEVIAILAASFGLLACIFFNKIYIILFKPSKNTIEEVRCSTAAHAFKVAARATLRRS
                                                                                                                                                            Q-----RCSTOKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium Sensing Receptor; CaSR; human; calcium level; modulator; hypotensive; osteopathic; receptor activity; hyperparathyroidism; osteoporosis; Paget's disease; treatment; hypercalcaemia malignancy;
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or osteoporosis.
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larity 74.0%; Pred. No. 0;
Conservative 86; Mismatches
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a subjected to pain and a subjected to pain, an actor of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity in an animal of one or more of the polypeptides or their activity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that paramaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence data for this patent did not form part of the printed for the specification) which is patent did not form part of the printed for the injury form in the sequence data for this patent did not form part of the printed for the injury form the form part of the printed for the injury form the pacetification but was obtained in electronic form directly from MIPO at the injury in the informance or the compound and the formance or the compound and the formance or the compound and the formance or the compound the formance or the compound the formanc
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                                                                                                                                                                     pain; neuronal tissue; gene therapy; segmental nerve injury; chronic constriction injury; CCI; nerve injury; SNI; Chung.
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                                                                                                                                    Human Protein P41180, SEQ ID NO 14277
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ADD48571 standard; protein; 1078
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765
                                                                                        (first entry)
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spinal segmental
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                                                                                                                                                                                                                                                                          Homo sapiens
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Ouery Match

Ouery Match

Dest Local Similarity 74.0%; Pred: No. 0;

Matches 782; Conservative 86; Mismatches

QORSQQQPRCK-QKVIFGSGTVTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRH- 1010 116 240 120 180 176 236 300 360 356 420 480 540 840 296 412 472 532 900 592 099 652 720 712 780 772 832 900 892 931 952 984 26 SVECIRYNPRGFRWLQAMIFAIEEINSSPALLPNLTLGYRIFDTCNTVSKALEATLSFVA ONKI DSLINLDEFCINCSEHI PSTIAVVČATGSGVSTAVANLLGLFYI PQVSYASSSRLLSN MAFYSCCWVLLALT ----WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE ATKCIRYNFRGFRWLQAMIFAIEEINNSWTFLPNITLGYRIFDTCNTVSKALEATLSFVA QNKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFY1PQVSYASSSRLLSN KNEYKAFLRTI PNDEQQATAMAEI I EHFQWNWVGTLAADDDYGRPGI DKFREEAVKRDI C IDFSEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS EAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWEETF HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLNFTNN MGEQVIPDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG FSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPGGFYSDETDASACNKCPDDFWSN LLLFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFBAKIPT SFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHEGSLMA VSAVEVIALLASSFGLLGCIYFNKCYIILFKPCRNTIBEVRCSTAAHAFKVAARATLRRS --LIMEM Q-----RCSTOKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKBFWEETF NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT MGEQVDFDDQGDLKGNYT1INWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKK1LWSG ENHTSCIAKEIEYLSWTEPPGIALTIFÄVLGILITSFVLGVFIKFRNTPIVKATNRELSY LLLFSLICCFSSSLIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPT SLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMA LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAVASTYGKF FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN DQGPPQKCEPQPANDARYKAAPTKGTLESPGGSKERP 1021 901 AASRKRSSSLCGSTISSPASSTCGPG-61 357 953 117 181 177 241 237 301 297 421 181 473 533 593 653 713 773 841 833 361 413 541 601 661 721 781 932 985 à 임 8 g ò g ò Вþ δ g à g 8 du à g & 9 & 9 19 6 6 6 g & g 8 셤 Д à δ 임

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51; Gaps

DB 7; Length 1078; 138; Indels 51; 1 MAQLHCQLLFLGFTLLQSYNVSGYGPNQRAQKKGDILLGGLFPIHFGVAAKDQDLKSRPE 60

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893 NVSRKRŠSLGGSTGSTPSSISSKSNSEDPFPQPERQKQQQPLALTQQEQQQQPLTLPQ 952
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                                          61 ATKCIRYNFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA
                                                              SUBCIRYNFRGFRWLQAMIFAIBEINSSPALLPWLTLGYRIFDTCNTVSKALEATLSFVA
                                                                                                                        ONKIDSLALDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                  pain; neuronal tissue; gene therapy; segmental nerve injury; CCI; nerve injury; SNI; Chung.
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                                                                                                                              Human Protein P41180, SEQ ID NO 8072.
    ADE62143 standard; protein; 1078
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; P41180.
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Matches 782; Conservative

Similarity

1 MAQLHCQLLFLGFTLLQSYNVSGYGPNQRAQXKGDILLGGLFPIHFGVAAKDQDLKSRPE 60

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412 480 472 540 532 900 592 099 652 720 712 780 772 840 832 900

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180 176

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1 MAFYSCCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                     Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                         Human Protein P41180, SEQ ID NO 8076
ADE62147 standard; protein; 1078 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                            14-AUG-2002; 2002WO-US025765
                           (first entry)
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                                                                                   Homo sapiens
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Costigan M;

Befort K,

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also which is differentially response in a animal subjected to pain and a subjected to pain and a subjected to pain and a subjected to pain, an artay, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the intentifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the cativity in an animal of one or more of the pain and a pharmaceutical composition, a cativity in an animal of one or more of the pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more oplypeptides or their antibodies. The polymodicatide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI) and spared nerve injury (SMI) in an animal (e.g. gene the respectification) which is patent did not form pret of the printed the specification, but was obtained in electronic form directly from WIPO at the function of the composition o
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Claim 1; Page; 1017pp; English.
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953 QQRSQQQPRCK-QKVIFGSGTVTFSLSFDBPQKNAMAHRNSTHQNSLBAQKSSDTLTRH- 1010
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                    SVECIRYNFRGFRWLQAMIFAIEBINSSPALLPNLTLGYRIFDTCNTVSKALEATLSFVA
                                                           QNKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN
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DB 7; 138;

74.8%; Score 4044.5; 74.0%; Pred. No. 0; tive 86; Mismatches

Conservative

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Similarity

Query Match Best Local Si Matches 782,

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Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
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                                                                                                                                                            HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS
                                                                                                                                                                                    LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF
                       EAWASSSLIAMPOYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWEETF
                                                                                                             NCHLOEGAKGPL---PVDTFLRGHEESGDRFSNS-STAFRPLCTGDENISSVETPYIDYT
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    DOGPPOKCEPOPANDARYKAAPTKGTLESPGGSKERP 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises the amino acid and coding sequences of polyvalent cation sensing receptor (PVCR) proteins from Atlantic salmon. The DNA and protein sequences of the invention are useful in the commercial raising of Atlantic salmon and the restoration of wild Atlantic salmon populations, especially in the transfer from freshwater to seawater with increased growth and reduced mortality. The present amino acid sequence represents the human parathyroid calcium receptor (HuPCaR) protein.
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                                                                                                                                                                                      polyvalent cation sensing receptor; PVCR; Atlantic salmon; growth increase; mortality reduction; human;
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                                                                                                                                            Human parathyroid calcium receptor (HuPCaR) protein
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Best Local Similarity 74.0%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches
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18-APR-2002; 2002US-00125772.
18-APR-2002; 2002US-00125778.
18-APR-2002; 2002US-00125792.
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Receptor; GPCR; G protein-coupled receptor; reproductive disorder; testicular disorder; vas deferens disorder; spermatogenesis; infertility; xm male; epididymitis; cryptorchidism; sperm transport disorder; testicular cancer; testicular germ cell tumour; male hormone disorder; premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder; inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity; graft-versus-host disease; actoimmunity disorder; systemic lupus erythematosus; drug induced haemolytic anaemia; sjogren's disease; T-cell maturation disorder; stroke; ischaemia; myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer; pulmonary disorder; brain disorder; endocrine disorder; ulcer;
                                  HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLHLKFTNS
                                                                                                              473 MGEQVIFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYNVYAKKGERLFINEEKILWSG
                                                                                                                                                    FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
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                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERAP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATKCIRYNFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120
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                                                                                                                                                                                                                                                                                       Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQIHCQLLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE
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                                                                                                                                                                                                     Glenn
                                                                                                                                                                                                       SW,
                                                                                                                                                                                                       Taylor
                                                                                                                                                                                                     Gibson BW,
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                                                                               12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                     Zhang
                                                                                                                                                 (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
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nes 782; Conserv
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Ramanathan CS 13-MAY-2003; 2003US-00436715 14-MAY-2002; 2002US-0380336P Mintier G, (RAMA/) RAMANATHAN C WPI; 2004-122081/12 (FEDE/) FEDER J N. (MINT/) MINTIER G. US2004018976-A1 29-JAN-2004 Feder JN, New

human G-protein coupled receptor polypeptide and polynucleotide, inl for diagnosing, preventing, treating or ameliorating a medical lition, e.g. reproductive disorder, immunodeficiency disease or useful for condition.

Disclosure; SEQ ID NO 74; 290pp; English.

The invention relates to an isolated human G protein-coupled receptor polypoptide and its encoding polyhuchcoride, including the full length proteins minus the start methionine (and the region of the polyhuchcolide condition than the protein region). The proteins are designated HGRBW13-1, HGRBW14-1, HGRBW14-2, HGRBW14-1, HGRBW14-1, HGRBW14-1, HGRBW14-2, HGRBW14-1, HGRBW14-1, HGRBW14-1, HGRBW14-2, HGRBW14-1, HGRBW14-1, HGRBW14-2, HGRBW14-1, HGRBW14-1, HGRBW14-1, HGRBW14-2, HGRBW14-1, HGGRBW14-1, HGGRBW14-

DB Score 4044.5; 74.88;

Sequence 1078 AA;

ζ. 360 420 412 480 472 540 900 9 652 720 780 840 900 892 984 61 ATKCIRYNFRGFRWLQAMIFAIBEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120 SUBCIRYNFRGFRALQAMIFAIEEINSSPALLPNLTLGYRIFDTCNTVSKALEATLSFVA 116 180 240 300 356 772 832 ONKIDSLALDEFCACSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSN 176 09 26 HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN VSAVEVIAILAASFGLLACIFFNKIYIILFKPSRNTIEEVRCSTAAHAFKVAARATLRRS XNEYKAFLRTIPNDEQQATAMAEIIEHFQWWWGTLAADDDYGRPGIDKFREEAVKRDIC IDFSEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG MGEQVIFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN LLLFSLICCFSSSLIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPT SLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMA SFHRKWWGLNLQFLLVFLCTFWQIVICVIWLYTAPPSSYRNQELEDEIIFITGHEGSLMA LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF 841 VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIBEVRCSTAAHAFKVAARATLRRS -----RCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH MAQLHCQLLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE ENHISCIAKEIEYLSWIEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 1 MAFYSCCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE QNKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN Gaps Indels DOGPPOKCEPOPANDARYKAAPTKGTLESPGGSKERP 1021 ed. No. 0; Mismatches 138; 86. 74.0%; Conservative Local Similarity 782; 357 57 121 117 181 177 237 301 297 361 413 481 473 541 533 601 593 661 653 721 713 781 773 901 932 953 985 241 421 Matches 셤 셤 셤 ò g ò 셤 qq à g ò g à 원 ò δ δ qq 음 ઠે 셤 ò g 8 임 ₹ 9 ò 임 ò ò d ò 8

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US-09-619-353-14
US-08-687-289A-7
US-09-435-897-7
US-08-943-986-8
US-08-153-784-8
US-08-484-159-8
US-09-655-481-4
US-09-655-481-4
US-09-619-897-6
US-09-435-897-6
US-09-435-897-5
US-09-619-353-10
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100.0%; Score 5410;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches
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1 MAQLHCQLLFLGFTLLQSYN......KGTLESPGGSKERPTTMEET
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1. /cgn2 6/ptodatca1/iaa/5A_COMB.pep:*

2. /cgn2 6/ptodatca1/iaa/5B_COMB.pep:*

3. /cgn2 6/ptodatca1/iaa/6A_COMB.pep:*

4. /cgn2 6/ptodatca1/iaa/6B_COMB.pep:*

5. /cgn2 6/ptodatca1/iaa/PCTUS COMB.pep:*

5. /cgn2 6/ptodatca1/iaa/PCTUS COMB.pep:*

6: /cgn2 6/ptodatca1/iaa/PCTUS COMB.pep:*
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Compugen Ltd.
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US-0148-588-7
US-08-485-588-7
US-08-484-565-7
US-08-484-719B-7
US-08-484-719B-7
US-08-484-719B-6
US-08-484-719B-7
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-08-480-751-8
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                                    GenCore version (c) 1993 - 2004
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 LENGTH: 1027
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APPLICANT: Harris, H. William
APPLICANT: Jury, Steven
APPLICANT: Jury, Steven
APPLICANT: Jury, Steven
APPLICANT: Nearing, Jacqueline A
APPLICANT: Brown, Edward M
APPLICANT: Brown, Edward M
TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
FILE REPERENCE: 2213.2004-001
CURRENT APPLICATION NUMBER: US/10/268,051
CURRENT APPLICATION NUMBER: US/10/268,051
CURRENT APPLICATION NUMBER: C0/328,464
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
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; Sequence 8, Application US/10268051
; Patent No. 6748900
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                                 RESULT 4

US-08-485-588-7

Squence 7, Application US/08485588

Patent No. 5688938

GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TILLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
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US-09-134-513-2

US-09-134-513-2

Sequence 2 Application US/09134513

Fatera No. 6210964

Fatera No. 6210964

FAPLICANT: Bar, Nuben

APPLICANT: Bar, Nuben

APPLICANT: Bar, Nuben

APPLICANT: Culum, Stephen J.

TITLE OF INVENITON: The Avian Extracellular Calcium-Sensing

TITLE OF INVENITON: Receptor

NOMBER OF SEQUENCES: 2

CONFESSORESEE: Vinson & Elkins L.L.P.

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STRIEE: D.C.

CONFUTER: IMM PC compatible

CONFUTER: IMM PC compatible

CONFUTER: IMM PC compatible

CONFUTER: ENABABLE FORM:

MEDIUM TYPE: IMM PC compatible

SOSTWARE: BARDABLE FORM:

MEDIUM TYPE: BRIGHTON

MEDIUM TYPE: US/09/134,513

FILING APPLICATION NUMBER: 105/09/134,513

TELEPANE: SALZO. ANGENEE NAME NOW 2:

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE THRADEBLES: NO CELEVANT

TELEPANE: ALLOS AMINO ACIGS

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE THRADEBLES: CONTINUED ACIGS

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE THRADEBLES: CONTINUED ACIGS

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SEQUENCE THRADEBLES: CONTINUED ACIGS

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                                                                      PITMEET 1027
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1021 PTTMEST 1027
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                                                                                                  NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT
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Patent No. 5763569
GENERAL INFORMATION
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TILLE OF INVENTION: MOLECULES
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
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633 West Fifth Street
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STREET:
CITY: LO
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US-08-484-565-7
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PRIOR APPLICATION NUMBER:
PRIVING DATE:
10 Cotober, 1994
APPLICATION NUMBER:
PRIVING DATE:
21 October, 1994
APPLICATION NUMBER:
PRIVING DATE:
22 APPLICATION NUMBER:
PRIVING DATE:
23 August, 1994
APPLICATION NUMBER:
PRIVING DATE:
25 August, 1993
APPLICATION NUMBER:
PRIVING DATE:
27 REDATA:
PRIVING DATE:
28 REDATA:
PRIVING DATE:
21 REDATA:
PRIVING DATE:
21 AUGUST, 1993
APPLICATION NUMBER:
PRIVING DATE:
21 AUGUST, 1992
APPLICATION NUMBER:
PRIVING DATE:
23 AUGUST, 1991
ATTORNEY/ARGATY INFORMATION:
NUMBER:
PRIVING DATE:
25 AUGUST, 1991
ATTORNEY/ARGATY INFORMATION:
NUMBER:
PRIVING DATE:

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                                                                                                                                                                     δ
                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Suite 4700
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38,179
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TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1078 amino acids
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.99
Matches 781; Conservative
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                                              Los Angeles
California
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                                                                      STATE: C
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                                                               NCYFIEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRTALRHPCTGEENITSVETPYLDYT
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Sequence 7, Application US/08480751
Fatenat No. 585684
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: Forrest H. Fuller
APPLICANT: Forrest H. Fuller
APPLICANT: Forrest H. Fuller
APPLICANT: Ames B. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sirist Interstate World Center
STREET: Suite 4700
STREET: Gallenia
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STATE: California

CONDITY: USA

ZIP. 90071

EDDIUM TYPE: 3.5 Diskette, 1.44 Mb storage COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Diskette, 1.44 Mb storage COMPUTER: PACTORIO PROPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACION DATA: PRIOR APPLICATION DATA: Including application PRIOR APPLICATION NUMBER: 08/353 784

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/29,827

FILING DATE: 22 October, 1994

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 08/01,127

FILING DATE: 11 February, 1993

APPLICATION NUMBER: U.S. 07/494,451

FILING DATE: 21 AUGUST, 1991

ATTORNEY/AGNIT INFORMATION:

APPLICATION NUMBER: U.S. 07/49,451

FILING DATE: 23 AUGUST, 1991

ATTORNEY/AGNIT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: U.S. 07/749,451

FILING DATE: 23 AUGUST, 1991

ATTORNEY/AGNIT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: U.S. 07/749,451

FILING DATE: 12 FEBRESCHE/DOCKET NUMBER: U.S. 07/749,451

FILING DATE: 13 489-1600

TELEBRAX: 67-3510

INFORMATION POR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENOTH: 1078 amino acids

TUSPOLICAT: 1078 amino acids

TUSPOLICAT: 1078 amino acids

TUSPOLICAT: 1078 amino acids

TOPOLOGY: 11near

MOLECULE TYPE: protein

US-08-484-565-7
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HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS
                                                                                                                 MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
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                                              NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT
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; Sequence 7, Application US/08943986
; Patent No. 596214
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: GALCIUM RECEPTOR.ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; NUMBER OF SEQUENCES: 20
; ADDRESSEE: Lyon & Lyon
STREET: Stiret interstate World Center
STREET: Stiret 1000
STREET: Stiret 4700
STREET: Galife...
CITY: Los Angeles
STATE: Calife...
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COMPUTER READABLE FORM:
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                                                                                                                                   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: 1BM PC compatible COMPUTER: PC-DOS/MS-DOS SOFTWARE: PASTSEQ CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/480,751 FILING DATE: 7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1078 amino acids amino acids
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.9%
Matches 781; Conservative
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                 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
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                                                                                                                                                                                                                    MGEQVIFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG
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                                        HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS
                                                                                                                                                                                         MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
                                                                                                                                                                                                                                                                                  541 FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
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           NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT
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Pagenence 7, Application US/08353784,
Patent No. 601068
GENERAL INFORMATION:
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Von Magenen,
APPLICANT: F. Balandrin, and Scott T. Moer TITLE OF INVENTION: CALCTUM RECEPTOR-ACTIVE TITLE OF INVENTION: CALCTUM RECEPTOR-ACTIVE TITLE OF INVENTION: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: Suite 4700
STREET: Los Angeles
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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STREET: 633 West Fi
CITY: Los Angeles
STATE: California
COUNTRY: USA
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                   storage
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb stc COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEG CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,986 FILING DATE: 03-OCT-1997 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/484,565 FILING DATE: 7-June-1995 APPLICATION NUMBER: 08/353,784 APPLICATION NUMBER: 08/353,784 APPLICATION NUMBER: US. 08/29/412117 FILING DATE: 21 October, 1994 APPLICATION NUMBER: U.S. 08/141,248 FILING DATE: 22 October, 1993 APPLICATION NUMBER: U.S. 08/141,248 FILING DATE: 22 Sectober, 1993 APPLICATION NUMBER: U.S. 08/017,127 FILING DATE: 12 February, 1993 APPLICATION NUMBER: U.S. 08/017,127 FILING DATE: 12 February, 1993 APPLICATION NUMBER: U.S. 07/834,044 FILING DATE: 12 Hobruary, 1993 APPLICATION NUMBER: U.S. 07/834,044 FILING DATE: 23 AUGUST, 1991 APPLICATION NUMBER: U.S. 07/49,451 FILING DATE: 23 AUGUST, 1991 APPLICATION NUMBER: U.S. 07/49,451 FILING DATE: 23 AUGUST, 1991 APPLICATION NUMBER: 38,179 APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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Best Local Similarity 73.9°
Matches 781; Conservative
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                                                                        MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
                                                                                                                                                       FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
                                                                                                                                                                                                                                 ENHISCIAKEIEYLSWIEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY
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APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Bradford C. Van Wagenen,
APPLICANT: Manuel F. Balandrin,
APPLICANT: Pricest H. Fuller, Eric G.
APPLICANT: Persest H. Fuller, Eric G.
APPLICANT: Carrest H. Ruller, Eric G.
APPLICANT: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: MS WORD
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STREET: First Interstate World Center
STREET: Suite 4700
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STATE: California
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CITY: L
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                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 1004
PRIOR APPLICATION DATA: 1004
APPLICATION NUMBER: CT/US/94/1217
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
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                                                                                                                                                                                                                                                                                                            FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY, AGGNT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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Best Local Similarity 73.9%
Matches 781; Conservative
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MOLECULE TYPE: protein
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                           HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS
                                                 HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLNFTNN
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                                                                                                     MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
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US-08-484-159-7
Sequence 7, Application US/08484159
Patent No. 631346
GENERAL INFORMATION:
APPLICANT: Bradford C. Van Wagenen
APPLICANT: Bric G. Del Mar
APPLICANT: Edward F. Balandrin
APPLICANT: Edward F. Nemeth
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOJECULES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: Suite 4700
STREET: Galifornia
CITY: Los Angeles
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
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SOFTWARE: FREESED for Windows Version 3.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,719B
FILING DATE: 7 June, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/353,784
FILING DATE: 2 October, 1994
APPLICATION NUMBER: US. 08/141,248
FILING DATE: 23 August, 1994
APPLICATION NUMBER: US. 08/141,248
FILING DATE: 23 February, 1993
APPLICATION NUMBER: US. 08/017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: US. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 21 August, 1991
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TUBER: Amino acids
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STRANDEDNESS: single
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Best Local Similarity
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413 HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN
                                                                                                       541 FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
                                                                                                                         653 ILLESLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKINRVLJVFBAKIPT
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                                 MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
                                                                 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG
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| Patent No. 5688938 |
| GENERAL INFORMATION: |
| APPLICANT: Edward M. Brown |
| APPLICANT: Steven C. Hebert |
| APPLICANT: Forrest H. Fuller |
| APPLICANT: James E. Garrett, Jr. |
| APPLICANT: James E. Garrett, Jr. |
| TILLE OF INVENTION: MOLECULES |
| NUMBER OF SEQUENCES: 20
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First Interstate World Center
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APPLICATION NUMBER: US/08/485,588
FILLING DATE: 7 June, 1995
CLASSIFICATION: 435
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SYSTEM: PC-DOS/MS-DOS
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
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: California
RY: USA
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SOFTWARE: FASTSEO
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STREET:
CITY: LO
STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139; Indels
                  CLASSIFICATION: ...
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 9 PRIOR APPLICATION DATA: described below: 9 APPLICATION NUMBER: 08/353,784 FILING DATE: 9 December, 1994 FILING DATE: 9 PECT/US/94/12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
74.6%; Score 4037.5;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 781; Conservative 86; Mismatches
                                                                                                       FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                                   PILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                            11 February, 1992
UMBER: U.S. 07/749,451
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11 February, 19;
APPLICATION UNMBER: 0.5, 07/
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   38,179
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TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // MOLECULE TYPE: protein US-08-484-159-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Sequence 6, Application US/08484565

Patent No. 5763569

GENERAL INFORMATION:
APPLICANT: Behard M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James B. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: First Interstate World Center
STREET: First Interstate World CITY: Los Angeles
CITY: Los Angeles
STREET: G33 Weet Fifth Street
CITY: Los Angeles
COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQLHCOLLFLGFTLLQSYNVSGYGPNQRAQKKGDIJLGGLFPIHFGVAAKDQDLKSRPE
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                                              application
below: 9
PRIOR APPLICATION DATA:
PRIOR PAPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
BELLING DATE:
BELI
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TELERY: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENDITH: 1088 amino acids
TYPE: amino acid
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Best Local Similarity 73.3
Matches 782; Conservative
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                                    ITCDEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFI
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                                                                                                            VKATNRELSYLLLFSLICCFSSSLIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRV
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                                                                                          591 TKCPNDFWSNENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPI
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Patent No. 5858684
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: Forest H. Fuller
APPLICANT: Games E. Garrett, Jr.
TITLE OF INVENTION: GALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: GALCIUM RECEPTOR-ACTIVE
TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891 VAARATLRRSAASRKRSSSLCGSTISSPASSTCGPG--
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
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APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Los Angeles
California
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US-08-480-751-6
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                                                FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/011,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 August, 1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 OCLOHAT
                                                                                                                                                                                                                                                                                                                                                            NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REPERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
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Best Local Similarity 73.3%
Matches 782; Conservative
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                                                                                                                                                                              LLVFEAKIPTSLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIF
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US-08-943-986-6
Sequence 6, Application US/08943986
Sequence 7, Application US/08943986
Patent No. 596314
GENERAL INFORMATION:
APPLICANT: Beward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Jacker B. GALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Silte Interstate World Center
STREET: Silte 4700
STREET: Silte 4700
STREET: Silte 4700
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FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/53,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/08/94/12117
FILING DATE: 21 October, 1994
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTEEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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STREET: Suite 4700
STREET: 633 West Fi
CITY: Los Angeles
STATE: California
COUNTRY: USA
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FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 1 October, 1994
APPLICATION NUMBER: U.S. 08/29,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/834,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 1 February, 1992
APPLICATION NUMBER: U.S. 07/49,451
FILING DATE: 23 August, 1991
APPLICATION NUMBER: U.S. 07/49,451
FILING DATE: 23 August, 1991
APPLICATION NUMBER: 213/004
FILING DATE: 23 August, 1991
APPLICATION NUMBER: 213/004
TELEFAM: 67-3510
TELEFAM: 67-3510
TELEFAM: 67-3510
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-480-751-6
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953 QQQQPLTLPQQQRSQQQPRCK-QKVIFGSGTVTFSLSFDEPQKNAMAHRNSTHQNSLEAQ 1011
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                                                                                                                                                                                                                                                                                                                  773 ITCHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNBAKFITFSMLIFFIVWISFI
                                                                                                                                                                                   LLVFEAKIPTSLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIF
                                593 NKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTFI
                                                                                                                                       VKATNRELSYLLLFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRV
                                                                                                                                                                                                             LLVFEAKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIF
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                                                                                               VKATNRELSYLLLFSLICCFSSSLIFIGEPRDWTCRLROPAFGISFVLCISCILVKTNRV
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFCATION: 514
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
APPLICATION DATA: including application
APPLICATION NUMBER: PCT/US/94/12117
APPLICATION NUMBER: US. 08/12117
FILING DATE: 23 August, 1994
FILING DATE: 23 August, 1994
APPLICATION NUMBER: US. 08/141,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDESSEE: Lyon & Lyon STREET: First Interstate World Center STREET: Suite 4700
STREET: 633 West Fifth Street CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-353-784-6
; Sequence 6, Application US/08353784
; Patent No. 6011068
; GENERAL INFORMATION:
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MEDIUM TYPE: 3.5" Di
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STATE: California
COUNTRY: USA
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FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/000,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/011,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 13 August, 1992
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 31,79
REPERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1088 amino acids
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Best Local Similarity 73.33
Matches 782; Conservative
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FSREPLTFVLSVLQVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECVDGEYSDETDASAC
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PILLING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 13 August, 1991

ATTORNEY/AGART INFORMATION:
NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REGISTRATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFRAM. (213) 955-0440

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERSTICS:
LENGTH: 1088 muino acids

TYPE: amino acid

TYPE: amino acid
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Best Local Similarity 73.3
Matches 782; Conservative
                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-784-6
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Search completed: November 17, 2004, 12:00:51 Job time : 131 secs

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1 MAQLHCQLLFLGFTLLQSYN......KGTLESPGGSKERPTIMEET 1027
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2: /cgn2_6/ptodata/1/pubpaa/PcT_NEW_PUB.Pep:*

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5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.Pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.Pep:*

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4 US-10-159-33-8

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US-10-436-715-24

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US-10-125-772-28

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US-10-725-778-8

US-10-725-778-9

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sequence 2, Application US/10125792

sequence 2, Application US/10125792

publication No. US20030051269A1

general INFORMATION:

APPLICANT: Matrical

APPLICANT: Nearing, Jacqueline A.

FILE REFERENCE: 2213.1006-007

CURRENT FILING DATE: 2002-06-16

PRIOR APPLICATION NUMBER: 10/121,441

PRIOR APPLICATION NUMBER: 60/240,392

PRIOR FILING DATE: 2000-10-11

PRIOR PILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

PRIOR SPELICATION NUMBER: 60/240,003

PRIOR SPELICANT: APPLICATION NUMBER: 60/240,003

PRIOR PAPEL SPECIAL NUMBER: 60/240,003
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches
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TYPE: PRT
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LENGTH: 1027
TYPE: PRT

OYGANISM: Squalus acanthias
US-10-125-778-2
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Matches 1027; Conservative
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             ATKCIRYNFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA
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RESULT 2 US-10-125-778-2 ; Sequence 2, Application US/10125778

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APPLICANT: Marries
APPLICANT: Marries
APPLICANT: Nearing, Jacqueline A.
APPLICANT: Nearing, Jacqueline A.
APPLICANT: Delyales
TITLE OF INVENTION: Polyalent Cation-Sensing Receptor in Atlantic Salm,
TILE FERENCE: 2213.106-005
CURRENT APPLICATION NUMBER: US/10/125,778
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 10/121,441
PRIOR APPLICATION NUMBER: 60/240,392
PRIOR FILING DATE: 2000-10-11
PRIOR FILING DATE: 2000-10-12
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RESULT 4
US-10-125-772-2
US-10-125-772-2
Sequence 2, Application US/10125772
Publication No. US2003012465741
GENERAL INFORMATION:
APPLICANT: Marrie, H. William
APPLICANT: Nearing, Jacqueline A.
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
FILE REPRENCE: 2213.1006-006
CURRENT APPLICATION NUMBER: US/10/125,772
CURRENT FILING DAIE: 2002-08-16
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ORGANISM: squalus acanthias
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PRIOR APPLICATION NUMBER: 10/121,441
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-10-11
PRIOR PILING DATE: 2001-10-11
PRIOR PELLOR NUMBER: 60/240,392
PRIOR PELLOR DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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PRIOR FILING DATE: 2000-10-12
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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; ORGANISM: Squalus acanthias
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Sequence 2, Application US/10410885

Publication No US20030232366A1

GABREAL INFORMATION

APPLICANT: Harris, H. William

APPLICANT: Betta, Marlies

ITILE REFERENCE: 2213.1066-008

CURRENT APPLICATION NUMBER: US/10/410,885

CURRENT FILING DATE: 2003-04-09

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 10/125,792

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: PCT/US01/31704

PRIOR APPLICATION NUMBER: PCT/US01/31704
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	QY 541 FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECNACAEGEFSDENDASACTKCPNDFWSN 600	Qy 601 ENHISCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660	QY 661 LLLFSLICCFSSLIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPT 720	QY 721 SLHRKWVGLNLQPLLLVPLCILVQIVTCIIWLYTAPPSSYRNHELBDEVIFITCDEGSLMA 780	OY 781 LGFLIGYTCLLAAICFFAFKSRKLPENPNEAKFITFSMLIFFIVWISFIPAYVSTYGKF 840	QY 841 VSAVEVIALLASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS 900 Db 833 VSAVEVIALLASFGLLACIFPNKIXIILFKPSRNTIEEVRCSTAAHAFKVAARATLRRS 992	ч е	93.2		C E ***********************************	KESULI 8 US-1159-339-8 ; Sequence 8, Application US/10159339 . Dublication No HS2003016654021) FULLICALUI NO. 035.03.02.03.02.03.03.03.03.03.03.03.03.03.03.03.03.03.	; IIILB OF INVENIEUR: HEFERMY30; FILE REFERENCE: D0169NP; CURRENT APPLICATION NUMBER: US/10/159,339; CURRENT FILING DATE: 2002-05-30;	; PRIOR APPLICATION NUMBER: US 60/294,411 ; PRIOR FILING DATE: 2001-05-30 ; NUMBER OF SEQ ID NOS: 9001-05-30 ; SOFTWARE: PatentIn version 3.1	; SEQ ID NO 8 ; LENGTH: 1078 ; TYPE: PRT ; ORGANISM: Homo sapiens	LU-159-339- Query Match Best Local S	TACUTES 702; CONSELVACIVE 00; MINNACCIES 100; INSCED 01; CAPO 1 MAQLHCQLEIGFILLQSYNVSGYGPNQRAQKGDIILGGLFPIHFGVAAKDQDLKSRPE 60	MARYSCCWVLLALITWHISANGPUQAAQANGALILLGGGLFFIHFGVAAANQULASAFE ATKCIRYNFRGFRWLQAMIFALEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA :::	Db 57 SVECIRYNFRGFRWLQAMIFALEBINSSPALLPNLTLGYRIFDTCNTVSKALEATLSFVA 116
841 VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS 900	901 AASRKRSSSLGGSTISSPASSTCGPGLIMEMQRCSTQKVSFGSGTVTLSLSFEETGRYAT 960 	961 LSRTARSRNSADGRSGDDLFSRHHDQGPPQKCEPQPANDARYKAAPTKGTLESPGGSKER 1020 	1021 PTIMEET 1027 1021 PTIMEET 1027	205-2		' INVENTION: MONKEY CALCIUM SENSING RECEPTOR PERENCE: GP-70665 APPLICATION NUMBER: US/09/727,205 FILING DATE: 2000-11-30	PRIOR APPLICATION NUMBER: 60/168,342 PRIOR FILING DATE: 1999-12-01 NUMBER OF SEQ ID NOS: SOFFWARE: FastESO for Windows Version 3.0	2 1078 RT	core 4055.5; DB 9; Length 1078; red. No. 4.2e-307;	85; Mismatches 136; Indels 51; Gaps	1 MAGLHCQLLFLGFTLLQSTNVSGYGFNQRAQKKGDILLGGLFFTHFGVAALUQLLKKFFF 60	61 ATKCIRYNPRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120 ::	121 ONKIDSLALDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN 180 	181 KNEYKAFLKTIPNDEQQATAMAEIIEHPQWNWYGTLAADDDYGRPGIDKFREEAVKRDIC 240 :: :	241 IDFSEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIMLAS 300 	301 EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF 360 	361 NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEBNITSVETPYLDYT 420	421 HERISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVFAWQVLNHLLHLKFTNS 480	

RECEPTOR,

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Pred. No. 3e-306;
5; Mismatches 138;
                                     60/380,336
FILE REFERENCE: D0262 NP
CURRENT APPLICATION NUMBER: US/10/-
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: U.S. 60/3
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 471
SEQ ID NO 22
LENGTH: 1078
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32; Conservative
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Publication No. US20040018976A1
GENERAL INFORMATION:
GENERAL INSTANTION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN
TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF
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SULT 10 -10-436-715-74 Sequence 74, Application US/10436715 Sequence 74, Application US/10436715 Sequence 74, Application US/10436715 GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RILLE REPERBENCE: DO262 NP TITLE OF INVENTION: NOWBER: US/10/436,715 CURRENT APPLICATION NUMBER: US. 60/380,336 PRIOR APPLICATION NUMBER: US. 60/380,336 PRIOR FILING DATE: 2002-05-14 NUMBER OF SEQ ID NOS: 471 SOFTWARE: Patentin version 3.2 LENGTH: 1078 TYPE: PRT ORGANISM: Homo sapiens	Db 653 İLİFŞİLĞCİRŞSİFFIGEPQDWTĞRLRQPARĞISFVLCISCILVKTURVLLVFEAKIPT QY 721 SLHRKWYGINLQPLLVFLCILVQIVTCIIMLYTAPPSSYRNHELEDEVIFITCDEGSLMA Db 731 SPHRKWMGINLQPLLVFLCTFWQIVICVIMLYTAPPSSYRNGELEDEIIFITCHEGSLMA QY 781 LGFLIGYTCLLAAICFFFAKSRLPENFNAKFITFSMLIFFIVWISFIDAVSYVGKF Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNAKFITFSMLIFFIVWISFIDAVSTYGKF QY 841 VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEFVKCSTAAHAFKVAARATLARS Db 933 VSAVEVIAILAASFGLLGCIYFNKIYIILFKPSRNTIEFVKCSTAAHAFKVAARATLARS QY 901 AASRKRSSSLCGSTISSPASSTCGPG	LCISCILVKTURVLIVFBAKIPT 712 SYRNHELEDBUIFITCDEGSLMA 79 SYRNGELEDBIIFITCHEGSLMA 772 SMLIFFTVWISFIPAYVSTYGKF 840 SMLIFFTVWISFIPAYVSTYGKF 840 SMLIFFTVWISFIPAYVSTYGKF 832 SMLIFFTVWISFIPAYSTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SMLIFFTVWISFIPAYASTYGKF 832 SWLIFFTVWISFIPAYASTYGKF 832 SWLIFFTWWISFIPAYASTYGKF 832 SWLIFFTVWISFIPAYASTYGKF 832 SWLIFTVWISFIPAYASTYGKF 832 SWLIFTVWISFIPAYASTYGKF 832 SWLIFTVWISFIPAYASTYGKF 832 SWLIFTVWISFIPAYASTYGKF 832 SWLIFTVWISFIPAYASTYGKF
Ouery Match Query Match Query Match Best Local Similarity 74.8%; Score 4044.5; DB 15; Length 1078; Best Local Similarity 74.0%; Pred. No. 36-306; Matches 782; Conservative 66; Mismatches 138; Indels 51; Gaps 7; Qy MAQLHCQLLFLGFTLLQSYNVSGYGPNQRACKGDILLGGLFPIHFGVAAKDQDLKSRPE 60	H 00 1 C H H H & C H L L H	1042 LULAR CALCIUM-SENSING G PROTEIN-COUPLE
177 CNOPERSFIRITENDEHQATAMADIIENFRNWWGTIAADDDYGREGIEKFREEAEERDIC 236	S. SOFTWARE: PatentIn version 3.1 S. SOFTWARE: PatentIn version 3.1 JENGTH: 1078 TYPE: PRT ORGANISM: Homo sapiens 174.8%; Score 4044.5; DB 15; Length 1078; Best Local Similarity 74.8%; Pred. No. 3e-306; Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps QY MAQLHOCLETCGTILGSYNVSGYGPNQRAQKKGDILLGGLPPIHFGVAAKDODLKSRPE	DB 15; Length 1078; 65; 138; Indels 51; Gaps 7; 7; 11GGLPPIHFGVAAKDQDLKSRPE 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSKVVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
APPLICANT: Zahag, Bill D.
APPLICANT: Zahag, Bill D.
APPLICANT: Zahag, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Danie B.
TITLE OF INVENTION: IDENIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 600088.465
CURRENT FILING DATE: 2003.04-04
NUMBER OF SEQ ID NOS: 3077
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 171
LENGTH: 1078
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-171
                                                                                                                                                                                                                                                                                                                                                                             Length 1078;
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74.8%; Score 4044.5; DB 16; Lengt
Best Local Similarity 74.0%; Pred. No. 3e-306;
Matches 782; Conservative 86; Mismatches 138; Indels
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US-10-408-765A-171
Sequence 171, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.

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APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Capen P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: South Christine L.
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953 QQRSQQQPRCK-QKVIFGSGTVTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRH- 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 IDFSELISQYSDEEEIQHVVEVIQNSTAKVIVVFSSGPDLEPLIKEIVRRNITGKIWLAS
                                                                                  NCYFTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGBENITSVETPYLDYT
                                                                                                                                       HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVBAWQVLNHLLHLKFTNS
                                                                                                                                                                                             MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG
                                                                                                                                                                                                                                                  FSKVVPFSNCSRDCVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN
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US-10-225-567A-118
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                                                                                                  VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS 900
                                                                                                                                          --- LIMEM 931
                                                                                                                                                                    893 NVSRKRSSSIGGSTGSTPSSSISSKSNSEDPFPQPERQKQQQPLALTQQEQQQPLTLPQ 952
                                                                                                                                                                                                 Q-----RCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH 984
  SFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHEGSLMA 772
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US-10-002-854-2
| Sequence 2, Application US/10002854
| Publication No US2002013224A1
| GENERAL INPORMATION:
| APPLICANT: Scadden, David T.
| APPLICANT: Poznansky, Mark C.
| APPLICANT: Poznansky, Mark C.
| APPLICANT: Brown, Edward M.
| TILLE OF INVENTION: THE CAREEPTOR AS A MEDIATOR OF TILLE REFRENCE: MO765/7038/ERG/KA CURRENT FILING DATE: 2001-11-01
| PRIOR FILING DATE: 2000-11-01
| PRIOR FILING DATE: 2000-06-02
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: FastSEQ for Windows Version 3.0
| TARKET IN NO 2
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                                            LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKF
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74.7%; Score 4039.5; DB 13; Length 1078;
Best Local Similarity 73.9%; Pred. No. 7.4e-306;
Matches 781; Conservative 86; Mismatches 139; Indels 51;
                                                                                                                                                                                                                                                        985 DQGPPQKCEPQPANDARYKAAPTKGTLESPGGSKERP 1021
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                                                                                                                                            AASRKRSSSLCGSTISSPASSTCGPG-----
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LOCATION: (1)...(1078)
CTHER INFORMATION: Ca-sensing Receptor
US-10-002-854-2
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ORGANISM: Homo sapiens
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RESULT 15
US-10-673-888-1
; Sequence 1, Application US/10673888
; Publication No. US20040082588A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Ellen
; APPLICANT: Choy, Wai Nang
; APPLICANT: Choy, Wai Nang
; APPLICANT: Mirro, Elmer
; TITLE OF INVENTION: METHODS FOR TREATING DISORDERS OF CALCIUM HOMEOSTASIS
; FILE REFERENCE: COC1600-US
; CURRENT APPLICATION NUMBER: US/10/673,888
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
                    240
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Q-----RCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHH 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (537)..(546)
OTHER INFORMATION: deleted in human calcium ion sensing receptor vortex.
FEATURE:
NAME/KEY: VARIANT
OCCATION: (936)..(936)
OTHER INFORMATION: Q in human calcium ion sensing receptor variant PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: VARIANT
; LOCATION: (1000)..(1000)
; OTHER INFORMATION: G in human calcium ion sensing receptor variant
US-10-673-888-1
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74.5%; Score 4029.5; DB 15; Length 1088;
Best Local Similarity 73.3%; Pred. No. 4.5e-305;
Matches 782; Conservative 86; Mismatches 138; Indels 61;
                                                                                                 -----QPLLPLQCGETDLDLTVQETGLQGPVGGDQRP 1042
                                                                        985 DQGPPQKCEPQPANDARYKAAPTKGTLESPGGSKERP 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENHTSCIAKEIBELSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSY
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                                                                                                                                                                                              1 MAFYSCCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE
                                                                                                                                                                                                                                                   61 ATKCIRYNFRGFRWLOAMIFALEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA
                                                                                                                                                                                                                                                                                                                            QNKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 FSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEXSDETDASACNKCPDDFWSN
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                                                                                                                                     Gaps
                                                                                               DB 14; Length 1078;
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                                                                                           Query Match
Best Local Similarity 73.9%;
Matches 781; Conservative 86
              TYPE: PRT
GRGANISM: Homo sapiens
US-10-225-567A-118
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541 FSK------VVPFSNCSRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASAC 590
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                                                                                                                                                                                                                                                                                                     773 ITCHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFI 832
                                                                                                                                                                                                                                                                                                                                    891 VAARATLERSAASEKRSSSLCGSTISSPASSTCGPG------- 926
                    HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLHHLKFTNS 480
                                  MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG 540
                                                                           592
                                                                                                                                                       591 TKCPNDFWSNENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPI 650
                                                                                                                                                                   593 NKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPI 652
                                                                                                                                                                                                                                              LLVFEAKIPTSLHRKWYGLNLOFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIF 770
                                                                                                                                                                                                                                                        893 VAARATLRRSNVSRKRSSSLGGSTGSTPSSSISSKSNSEDPFPRPERQKQQQPLALTQQE 952
                                                                                                                                                                                                                                                                                                                                                                                                                            927 ----LITMEMQ-----RCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGR 974
357 NCHLQEGAKGPL---PVDTFLRGHEESGDRFSNS-STAFRPLCTGDENISSVETPYIDYT 412
                                                                                                                        975 SGDDLPSRHHDQGPPQKCEPQPANDARYKAAPTKGTLESPGGSKERP 1021
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November 17, 2004, 11:02:39; Search time 73 Seconds (without alignments) 1353.625 Million cell updates/sec
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1 MAQLHCQLLFLGFTLLQSYN......KGTLBSPGGSKERPTTMEET 1027
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

	Description		calcium receptor (Ca(2+)-sensing rec		metabotropic gluta							tabotropic	6		υ	taste receptor T1R	glutamate receptor	hypothetical prote	hypothetical prote	metabotropic gluta	hypothetical prote	ionotropic glutama	probable ligand-ga	probable ligand-ga	glutamate receptor	probable glutamate	ionotropic glutama	ligand gated chann	N-methyl-D-asparta
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probable ligand-ga	N-methyl-D-asparta	gamma-aminobutyric	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	N-methyl-D-asparta	probable glutamate	ligand gated chann	probable ligand-ga
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ALIGNMENTS

RESULT 1 A56715 calcium receptor (clone phPcaR-4.0) - human
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C;Accession: Abb/15; 349341; A49413; 249413; C49413 R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C
J. Biol. Chem. 270, 12919-12925, 1995 A.Title. Molecular cloning and functional expression of human parathoroid calcium recepts
7
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1078 <gar> A:Cross-references: GB:U20759; NID:q683744; PIDN:AAA86503.1; PID:g683745</gar>
R; Pearce, S.H.S.; Thakker, R.V.
submitted to the EMBL Data Library, August 1994 A beforence number: G40141
A.Accession: S49341
A;Status: preliminary
A.Rocidente Type: D.N.A. A.Rocidues: 1-180, 'O', 182-989, 'R', 991-1078 <pea></pea>
R.Pollak, M.R., Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, J
Leil 15, 1237-1203, 1353. Leil 15, 1237-1203, 1353.
A;Accession: A49419
A, Status: preliminary
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A, Experimental source: family N
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human parathyroid calcium recepto
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calcium receptor (clone phPCaR-5.2) - human

cispecies: Homo sapiens (man)

cispecies: Homo sapiens (man)

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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1088 <GAR>
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                                          ; Score 4037.5; DB 2; Length 1078; Pred. No. 2.8e-287; 86; Mismatches 139; Indels 51;
C, Keywords: glycoprotein; receptor; transmembrane protein
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                                          Query Match
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Calcium/polyvalent cation-sensing receptor precursor - rat
Calcium/polyvalent cation-sensing receptor precursor - rat
Cipecies Rattus norvegicus (Norway rat)
Cipace: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
Cipaces 10-159362; A55594
Rivat, M.; Molliver, M.B.; Snowman, A.M.; Snyder, S.H.
Rivat, M.; Molliver, M.B.; Snowman, A.M.; Snyder, S.H.
Rivation sensing receptor: molecular cloning in rat and localization to nerve terminates calcium sensing receptor: molecular cloning in rat and localization to nerve terminates: 159362; MUID:95241465; PMID:7724534
A;Reference number: 159362; MUID:95241465; PMID:7724534
A;Residues: translated from GB/BMBL/DDBJ
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A;Residues: 1-1079 cRES>
A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:g790578; PIDN:AAC52195.1; PID:g79057
A;Experimental source: striatal
R;Ricaracli, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
R;Ricaracli, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert and functional expression of a rat kidney extracellular calcium/polyvale
A;Reference number: A55594; MUID:95116508; PMID:7816802 1012 840 900 893 925 953 780 773 833 533 900 660 653 720 713 473 593 954 PSTPQPQPQSQQPPRCK-QKVIFQSGTVTFSLSFDEPQKTAVAHRNSTHGTSLEAQKNND SFHRKWMGLNLOFILLVFLCTFMQIVICAIWLNTAPPSSYRNHELEDEIIFITCHEGSLWA IGELIGYTCLIAAICPFFAKSRKLPENFNEAKFITFSMLIPFIVWISFIPAYVSTYGKF LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIUWISFIPAYASTYGKF VSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRS GLTMEMO------RCSTOKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDD STHRKWYGINLOFILVFICILVQIVTCIIWLYTAPPSSYRNHELEDBVIFITCDEGSLMA 474 MGEQVIFDECGDLAGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINDEXILWSG FSKVVPFSNCSRDCVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSN LLLFSLICCFSSSLIFIGEPROWTCRLROPAFGISFVLCISCILVKTNRVLLVFBAKIPT MGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSG ENHISCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY NCHLOEGAKGPL---PVDTFLRGHEEGGARLSNS-PTAFRPLCTGEENISSVETPYMDYT HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVINHLLHLKFTNS protein A;Accession: A55594
A;Molecule type: mRNA
A;Residues: 1-133,'X',135-1079 <RIC>
A;Residues: 1-133,'X',135-1079 <RIC>
A;Residues: 1-133,'X',135-1079 <RIC>
C;Keywords: references: GB:U10354
A;Experimental source: kidney
C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane 1013 ALTKH-----QALLPLQCGETDSELTSQETGLQGPVG-EDHQLEMED LPSRHHDOGPPOKCEPQPANDARYKAAPTKGTLESPGGSKERPTTMEE 901 AASRKRSSSLCGSTISSPASSTCG--------414 541 594 661 654 721 714 781 774 841 834 894 926 979 481 601 421 RESULT g g 8 6 B 6 8 G 8 ò g ò g 3 g 8 9 8 B 8 g ò RESULT 3
\$40476
Ca(2+)-sensing receptor - bovine
CiSpecies: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; Harters 366, 575-580, 1993
A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from ba; A;Tecters number: \$40476
A;Accession: \$40476
A;Accession: Stoliminary
A;Status: preliminary
A;Status: Preliminary
A;Status: Preliminary
A;Status: Dreliminary
A;Status: Dreliminary
A;Cross-references: UNIPROT: P935384; GB:S67307; NID:G453108; PIDN:AAB29171.1; PID:G453109 120 117 180 240 297 237 300 360 NCYFTEKTLIQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420 177 PAYVSTYGKFVSAVEVIALLASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFK 890 VKATNRELSYLLLFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRV 712 9 57 ATKCIRYNFRGFRWLQAMIFAIBBINNSMTFLPNITLGYRIFDTCNTVSKALBATLSFVA 58 SVECIRVNFRGFRMLQAMIFAIBEINSSPALLFNWTLGYRIFDTCNTVSKALEATLSFVA KNEYKAFLRTI PNDEQQATAWAEIIEHFQWNWVGTLAADDDYGRPGIDKFREEAVKRDIC IDFSEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS ----LTMEMQ-----RCSTQKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGR 1 MAQLHCQLLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE ONKIDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN EAWASSSLIAKPEYPHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF ITCDEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFI Query Match 73.9%; Score 3999.5; DB 2; Length 1085; Best Local Similarity 72.8%; Pred. No. 1.7e-284; Matches 778; Conservative 92; Mismatches 141; Indels 57; Gaps KSSDTITRH-----QPLLPLQCGETDLDLTVQETGLQGPVGGDQRP 1052 SGDDLPSRHHDOGPPOKCEPOPANDARYKAAPTKGTLESPGGSKERP 1021 VAARATLRRSAASRKRSSSLCGSTISSPASSTCGPG--118 181 178 241 238 301 121 361 773 833 891 927 953 975 61 831 893 711 713 771 상 Ω q d Db 임 ŏ δ $\overset{\circ}{\circ}$ $\dot{\circ}$ 8 6 8 6 g ò ਨੇ ò 유 상 유 δ g

Page 4

F.11-20/DO F.18-635 F.613-635 F.650-670 F.7650-670 F.7650-670 F.7650-670 F.7660-670 F.7670-790 F.7670 F.7670-790 F.7670-790 F.7670-790 F.7670-790 F.7670-790 F.7670-7	0/Domain: signal sequence #status predicted <sig> -1212/Region: hydrophobic -635/Domain: transmembrane #status predicted <tm1> -670/Domain: transmembrane #status predicted <tm2> -700/Domain: transmembrane #status predicted <tm2> -744/Domain: transmembrane #status predicted <tm3> -829/Domain: transmembrane #status predicted <tm5> -860/Domain: transmembrane #status predicted <tm6> -810/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted <tm6< th=""><th>QY 840 FVSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLAR 899 B32 FVSAVEVIAILAASFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHAFKVAARATLAR 891 QY 900 SAASRKRSSSLCGSTISSPASSTCOPG</th></tm6<></tm6></tm5></tm5></tm5></tm5></tm3></tm2></tm2></tm1></sig>	QY 840 FVSAVEVIAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLAR 899 B32 FVSAVEVIAILAASFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHAFKVAARATLAR 891 QY 900 SAASRKRSSSLCGSTISSPASSTCOPG
6 6 6 6 6	1 MAQLHCQLLFLGSTNVSGYGPNQRAQKKGDIILGGLPPIHFGVAAKDODLKSRPE 60	RESULT 5 JH0562 JH0562 Chostoric glutamate receptor 3 precursor - rat Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 Cispecession: JH0562 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 Cispecession: JH0561 # Ishii, T.; Shigemoto, R.; Nakanishi, S. A;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S. A;Title: A family of metabotropic glutamate receptors. A;Reference number: JH0561; MUID:92110002; PMID:1309649
666666	181 KNEYKAFLRTIPNDEQQATAMABIIEHFQWNWVGTLAADDDYGRPGIDKEREBAVKRDIC 240	A.Residues: 1-879 «TAN» A.Residues: 1-879 «TAN» A.Cross-references: UNIPROT:P31422 A.Cross-references: UNIPROT:P31422 A.Cross-references: UNIPROT:P31422 A.Crommental source: brain C.Superfamily: metabotropic glutamate receptor 4 C.Superfamily: metabotropic glutamate receptor 4 C.Superfamily: metabotropic glutamate receptor 3 F.1-22/Domain: signal sequence #status predicted <sig> F.3-879/Product: metabotropic glutamate receptor 3 #status predicted <met> F.51-529/Domain: transmembrane #status predicted <tii> F.614-634/Domain: transmembrane #status predicted <tii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.646-664/Domain: transmembrane #status predicted <iii> F.647-664/Domain: ></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></iii></tii></tii></met></sig>
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3 6 6 6 6	N O N O N C	OY 7 QLFLGTTL-LOSYNVGGYGPNORAGKKDDILGGGLFPHFGVARXDDLKSRPE 60 Db 8 QILMLALFSKGFLLSLGDHNFMRREIKIEGDLVLGGLFPHNEKGTG 53 QY 61 ATKCIRYN-FRGFRWLQAMIFALEEINNSMFELPHTLGKRFFDTCNTVSKALEATLSFV 119 Db 54 TEBCGRINEDRGIQRLEAMLFAIDEINNYLLPGVKLGVHLDTCSRDTYALEQSLEFV 113 QY 120AQNKIDSLNLDEFCNCSDHIPSTIA-VVGATGSGISTAVANLLGLFYIPQVSYAS 173 110 DAGNKIDSLNLDEFCNCSDHIPSTIA-VVGATGSGISTAVANLLGLFYIPQVSYAS 173 111 DAGNKIDSLNLDEFCNCSDHIPSTIA-VVGATGSGISTAVANLLGLFYIPQVSYAS 173
6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1	174 SSRLLSNKNEYKAFLKTIPNDEQQATAMAEIIEHFQWNWYGTLAADDYGRPGIDKFREE 174 TSAKLSDKSRYDYRANFYDEQQATAMAEIIEHFQWNWYGTLAADDYGRPGIDKFREE 175 TSAKLSDKSRYDYPEFYQAMAEIIEHFGWNWYGTVASEGDYGHET

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metabotropic glutamate receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JH0561
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Naucon 8, 169-179, 1992
A;Title: A family of metabotropic glutamate receptors.
A;Reference number: JH0561; MUD:92110002; PMID:1309649
A;Accession: JH0561
A;Reference number: JH0561; MUD:92110002; PMID:1309649
A;Accession: JH0561
A;Reference number: JH0561; MUD:92110002; PMID:1309649
A;Accession: JH0561
A;Reference number: JH0561; MUD:9210002; PMID:1309649
A;Accession: Lansmembrane #status predicted <IRI>F;601-655/Domain: transmembrane #status predicted <IRI>F;601-675/Domain: transmembrane #status predicted <IRI>F;701-792/Domain: transmembrane #status predicted <IRI>F;701-792/Domain: transmembrane #status predicted <IRI
F;701-792/Domain: transmembrane #status predicted <IRI
F;701-793/Domain: transmembrane #status predicted <IRI
F;701-793/Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAITFILISLOLGICVMFVVDP--SHSVVDFQDQRTLDPRFARGVLKCDISDL-SLICL 756
                             -YKVIGSWIDHLHLRIERMQWPGSGQQLPRSICSL 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 IGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKFVSAV 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EV-----IAILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARAT 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCVPGTRKGI1EGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSNENHTSC1AKE1E
                                                                                                                                                   523 PÓQPGERKKTVKG-MACCWHCEPCTGYQY--QVDRYTCKTCPYDMRPTENRTSCQPIPIV
                                                                                                                                                                                                               613 YLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSYLLLFSLICCFSS
                                                                                                                                                                                                                                                   580 KLEWDSPWAVLPLFLEAVVGIAATLFVVVTFVRYNDTPIVKASGRELSYVLLAGIFLCYAT
                                                                                                                                                                                                                                                                                                                                        SLIFIGEPROWTCRLROPAFGISFVLCISCILVKTNRVLLVFEAKIPTSLHRKWVGLNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               733 FLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIF------ITCDEGSLMALGFL
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                             RYDIYQYQLRNGSAE-
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R,Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

A;Title: A femily of metabotropic glutamate receptors.

A;Title: A femily of metabotropic glutamate receptors.

A;Reference number: JH0561; MUID:92110002; PMID:1309649

A;Reference number: JH0561; MUID:92110002; PMID:1309649

A;Residue: T.912 - C-RNA

A;Cross-references: UNIPROT:P31423

A;Residues: L.912 - C-RNA

A;Cross-references: UNIPROT:P31423

A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac A;Crossion: 15149

A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac A;Crossion: I5149

A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac A;Cross-references GB:M90518, MID:93332699; PMID:8338667

A;Reference maka.

A;Rolecule Type: mRNA

A;Rolecule Type: mRNA

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A;Rolecule Type: mRNA

A;Rolecule: L-123, YR, 1,25-912 cRES>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 LKWNYVSTLASEGSYGESGVEAFIQKSRENGGVCIAQSVKIPR--EPKTGEFDKIIKRLL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTIINWQL---SAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPFSNCSR 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NITLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSDHIP-
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                                                                                                                                                                                                       BATLSFV---AQNKIDSLNLDE-FCNCSDHIP-----STIAVVGATGSGISTAVANL
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                                                                                                                                                       1 MGRLPVLLLWLAWWLSQAGIACGAGSVRLA---GGLTLGGLPPVHARGAAGRACGALKKE
A, Experimental source: retina
A, Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBIP:133250)
C, Superfamily: metabotropic glutamate receptor 4
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                  rre 1108.5; DB 2; Length
cd. No. 8.6e-73;
Mismatches 356; Indels
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|GFDQYFMTRSLENNRRNIWFABFWEENFNCKLT-------
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Gebecies: Rattus norvegicus (Norway rat)
C, Baccies: Rattus norvegicus (Norway rat)
C, Baccies: Rattus norvegicus (Norway rat)
C, Baccies: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C, Accession: A46742
C, Accession: A46742
R, Nakajima, Y.; Iwakabe H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi
J, Biol. Chem. 268, 11866-11873, 1993
A, Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m
A, Reference number: A46742
A, Reference number: A46742
A, Status: preliminary
A, Status: preliminary
A, Status: J-871 chaks
A, Status: L-871 chaks
A, Cross-references: UNIPROT: P35349; GB: D13963; NID: G391856; PIDN: BAA03066.1; PID: G391857
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                                                                                                  SAKLSDKSRYDYFARTVPPDFFQAKAMAEILRFFNWTYVSTVASEGDYGETGIBAFELEA
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REFWEERFHCSFRQRDC--------AAHSLRAV---PFEQESKIMFV
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metabotropic glutamate receptor 8 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: Oz-Vul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149142
R;Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A;Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory by A;Reference number: 149142; MUID:95239344; PMID:7722646
A;Reference number: 149142; MUID:95239344; PMID:7722646
A;Accession: 149142
A;Accession: I49142
A;Accession: L908-xES>
A;Residues: 1-908 «RES>
A;Cross-references: UNIPROT:P47743; EMBL:U17252; NID:9854728; PIDN:AAA68149.1; PID:985472
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                                                                         SCIAKEIEYLSWIEPFGIALTIFAVLGILLITSFVLGVFIKFRNTPIVKATNRELSYLLLF
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Best Local Similarity 30.5%; Pred. No. 1.8e-70;
Matches 290; Conservative 176; Mismatches 363;
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C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor
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                         RESULT 10
A49874
metabotropic glutamate receptor 7 - rat
metabotropic glutamate receptor 7 - rat
metabotropic glutamate receptor 7 - rat

N.Alternate names: metabotropic glutamate receptor mGluR7
C'Species: Rattus norvegicus (Norway rat)
C'Species: Rattus norvegicus (Norway rat)
C'Species: Rattus norvegicus (Norway rat)
C'Accession: A49874; IS5984
S'Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi,
J. Biol. Chem. 269, 1231-1235, 1994
A; Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup
A; Reference number: A49874; MUID:94117433; PMID:8288585
A; Accession: A49874
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Saugstad, J.A.; Kinzle, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
MOI. Pharmacol. 45, 357-372, 1994
A; Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A; Reference number: IS7954; MUID:94195260; PMID:8145723
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-915 - RES
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: EMBL:U06832, NID:g459657; PIDN:AAA20655.1; PID:g459658 C;Genetics: A;Genetics: A;Genetics: C;Superfamily: metabotropic glutamate receptor 4 C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AIBEINNSMIFLPNITLGYRIFDICNTVSKALBATLSFVAQNKIDSLNLDEFCNCSDHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 ALDQINSDPNLLDENVTLGARILDICSRDTYALEQSLIFV-QALIQKDISD--VRCTNGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 YGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPEATKC---IRYNFRGFRWLQAMIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 YAPHS-IRIEGDVTLGGLFPVH----AKG-----PSGVPCGDIKREN--GIHRLEAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 915;
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               C--IRYNFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQ 121
                                                                               NKIDSLNLDEFCNCSDHIPST----IAVVGATGSGISTAVANLLGLFYIPQVSYASS
                                                                                                                                            SRLLSNKNEYKAFLRTIPNDEQQATAMAEIIEHFQWNWVGTLAADDDYGRPGIDKFREEA
                                                                                                                                                                                                                                                                                                VKEFWEETFNCY - - - FTEKTLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEEN
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                                                                                                                                                                  SMDLSDKTLFKYFMRVVVPSDAQQARAMVDIVKRYNWTYVSAVHTEGNYGESGMEAFKDMS
                                                                                                                                                                                                                                      AKEGICIAHSYKİYSNAGEQSFDKLKKLISHLPKARVVACFCEGMTVRGLLMAMRRLGL
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                                                                                                           SLISSEEBEGLVRCVDGSSSSFRSKKPIVGVIGPGSSSVAIQVQNLLQLFNIPQIAYSAT
                                                                                                                                                                                                             VKRDICIDFSEMISQYYTQKQLEFIADVIQN--SSAKVIVVFSNGPDLEPLIQEIVRRNI
                                                                                                                                                                                                                                                                             T-DRIWLASEAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGF
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"C12131

metabotropic glutamate receptor 5 B - human

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996

C;Accession: JC2131

R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A;Title: Molecular cloning and the functional expression of two isoforms of humar

A;Reference number: JC2131; MUID:94197696; PMID:7908515

A;Accession: JC2131

A;Rolecule type: mRNA

A;Residues: 1-1212 cMIN>
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane predicted cTM2>
F;644-664/Domain: transmembrane #status predicted cTM2>
F;644-664/Domain: transmembrane #status predicted cTM3>
F;694-714/Domain: transmembrane #status predicted cTM5>
F;773-794/Domain: transmembrane #status predicted cTM5>
F;773-794/Domain: transmembrane #status predicted cTM5>
F;803-827/Domain: transmembrane #status predicted cTM7>
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                                                              ------KRNSHIKKCTGLERIAR-DSS
                                                                                             YLDYTHLRISYNVYVAVYSIAHALQDIHS--CKPGTGIFANGSCADIKKVEAWQVLNHLL
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                                                                                                                                                               HLKFTNSMGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINE
                                                                                                                                                                                                                                                  EDMOWANREHTHPASVCSLPCKPGERKKTVKGVP-CCWHCGRC-EG-YNYQVDELSCELC
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779 880 837 933

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A.Residues: 1-1171 <ABE>
A.Cross-references: UNIPROT: P31424; GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d1002186
A.Cross-references: UNIPROT: P31424; GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d1002186
A.Stoperimental source: Drain
A.Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIP:107750)
C.Keywords: G protein-coupled receptor; transmembrane protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
J. Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 con
A;Reference number: A42916; MUID:92317054; PMID:1320017
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                                EGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYV
                                                                                                                                                                                                                   865 LPCRSNTFLNIFR-----RKKPGAGNANSNGKSVSWSEPGGRQAPKGQHV-WQRLSVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 SLISSEEEEGLVRCVDGSSSFRSKKPIVGVIGPGSSSVAIQVQNLLQLFNIPQIAYSATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 RILSNKNEYKAFLRTIPNDEQQATAMAEIIEHFQWNWVGTLAADDDYGRPGIDKFREEAV
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  LLLFSLICCFSSSLIFIGEPRDWTCRLROPAFGISFVLCISCILVKTNRVLLVF---EAK
                                                                                                                                                                                                                                                                                                                                                                                ---RCSTAAHAFKVAARATLRRSAASRKRSSSLCGSTISSPASSTCGPGLIMEMORCS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 NKIDSLNLDEFCNCSDHIPS-----TIAVVGATGSGISTAVANLLGLFYIPQVSYASSS
                                                                                             718 IPTSLHR----KWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCD
                                                                                                                                                                                                                                                                                   STYGKFVSAVEVIALLASSFGLLGCIYFNKCYIILFKPCRN-----TIEEV-----
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A;Residues: 1-1171 <A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQNKI-----DSLNLDEFCNC---SDH 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AQKKGDIILGGLFPIHFGVAAKDQDLKSRPEATKC--IRYNFRGFRWLQAMIFAIBEINN 87
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19.4%; Score 1052; DB 2; 1
al Similarity 28.6%; Pred. No. 1.9e-68;
296; Conservative 184; Mismatches 402;
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Best Local Similarity
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F;644-664/Domain: transmembrane #status predicted <tm3> F;694-714/Domain: transmembrane #status predicted <tm4> F;738-759/Domain: transmembrane #status predicted <tm5> F;738-759/Domain: transmembrane #status predicted <tm5> F;738-754/Domain: transmembrane #status predicted <tm5> F;803-827/Domain: transmembrane #status predicted <tm7> Query Match Query M</tm7></tm5></tm5></tm5></tm4></tm3>	: : :	OY 175 SRLLSNKUSYKAFLKTIPNDEQQATAMABIIEHFQWNWVGTLAADDDYGRPGIDKFREBA 20	3 5 2 6 3 5 2 6 3 5 5 2 6	QY 409 ITSVETPYLDYTHLRISYNVYVAVYSIAHALQDIH-SCKPGTGIFANGSCADIKKVEA 4	OY 526 SDRLNINEKKILWSGFSKVVPFSNCSRDCVFGTRKGIIEGEPTCCFECMACAEGEFSDEN S ::::	OY 646 RNTPIVKATNRELSYLLLFSLICCFSSSLIFIGEPROWTCRLRQPAFGISFVLCISCILV .	763 ELEDEVIFITCDEGSLMALGFLIGYTCLIAAICFFFAFKSRKLPENFAKE 724 PSIREV-YLLCNITNLOVUTPLGYNGLLILSCTFYAFKTRNVPANFNEAKE 603 FEBINAGELENGYLENGYPENGANGULIAFFFAFKSRNVPANFNEAKE	1 IFTIWALSE PAYOSITARY SANDAYALLASSIGLICOLITERACITIES CONTINES OF TACILMIAFVELY FESSIVALITE CONTINES OF TACILMIAFVELY FESSIVALITE CONTINES OF TACILMIAFVELY FESSIVALITE CONTINES OF TACILMIAFVELY CONTINES OF TACILMIAF CONTINES OF TACILMIA CON
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VARIANTS FHH GLN-185; LYS-297 AND TRP-795.
MEDLINE=94094324; PubMed=7916660;
Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,
Steinmann B., Levi T., Seidman C.E., Seidman J.G.;
"Mutations in the human Ca(2+)-sensing receptor gene cause familial
hypocalciunic hypercalcemia and neonatal severe hyperparathyroidism.";
Cell 75:1297-1303(1993). thyroid SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
MEDLINE=95403641; Pubmeda-7673400;
Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;
Familial hypocalciuric hypercalcemia associated with mutation in the Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J., Hebert S.C., Seidman C.E., Seidman J.G.; "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.; Changes in calcium responsiveness and handling during keratinocyte differentiation. Potential role of the calcium receptor."; J. Clin. Invest. 97:1085-1093(1996). MEDLINE-96343808; PubMed-8756555; Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V., Aida K., Koishi S., Tawata M., Onaya T.; "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from SEQUENCE FROM N.A.
TISSUE=Parathyroid;
MEDLINE=PS279439; PubMed=7759551;
MEDLINE=95279439; PubMed=7759551;
MEDLINE=95279439; Pubmed I.V., Hammerland L.G., Hung B.C., Brown E.M. Hebert S.C., Nemeth E.F., Fuller F.;
Molecular cloning and functional expression of human parathyroid "Expression of a calcium-sensing receptor in a human medullary thy carcinoma cell line and its contribution to calcitonin secretion." Endocrinology 137:3842-3848(1996). Seidman J.G. Seidman C.E., "Mutations in the human $\operatorname{Ca}(2+)$ -sensing-receptor gene that cause MEDLINE=9524322; PubMed=7726161; Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidm VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227. Pearce S.H.S., Thakker R.V.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases. Biochem. Biophys. Res. Commun. 214:524-529(1995) familial hypocalciuric hypercalcemia. calcium receptor cDNAs."; J. Biol. Chem. 270:12919-12925(1995) SEQUENCE OF 643-908 FROM N.A. MEDLINE=96193893; PubMed=8613532; MEDLINE=95408281; PubMed=7677761; MEDLINE=95179179; PubMed=7874174; Genet. 8:303-307(1994).

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                                                                                                                                                                                                                                                                                                             "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated with familial hypocalciuric hypercalcemia."; Hum. Mutat. 10:233-235(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTH levels.

DiSEASE: Defects in CASR are the cause of neonatal severe primary bygerparathyroidism (NSHPT) [MIM:239200]; in which the receptor has reduced activity. NSHPT is a rare autosomal recessive lifethreatening disorder characterized by very high serum calcium concentrations, skeletal demineralization, and parathyroid hyperplasia. In some instances NSHPT has been demonstrated to be the homozygous form of FHH.

DiSEASE: Defects in CASR are the cause of autosomal dominant hypocalcemia (ADH) [MIM:601108]; in which the receptor is activated at subnormal Ca(2+) levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=P41180-2; Sequence=VSP 002035;
TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
liver, heart, skeletal muscle, or placenta.
DISEASE: Defects in CASR are the cause of familial hypocalciuric
hypercalcemia, type 1 (FHH) [MIM:45980]; in which the receptor
hypercalcemia, type 1 (RH) [MIM:45980]; in which the receptor
homeostasis. Affected individuals exhibit mild or modest
hypercalcemia, relative hypocalciuria, and inappropriately normal
                                                                                                                                                                                                                                                                                                                                                                     VARIANT FIH VAL-616.
MEDLINE=99415602; PubMed=10487661;
Stock Ji., Baron J., Coderre J.A., Mancilla E.,
De Luca F., Ray K., Mericq M.V.;
"Autosomal dominant hypoparathyroidism associated with short stature and premature osteoarthriis.";
J. Clin. Endocrinol. Metab. 84:3036-3040(1999).
                                                                                                 "Calcium-sensing receptor mutations in familial benign hypercalcemia and neonatal hyperparathyroidism.", J. Clin. Invest. 96:2683-2692(1995).
                                                                                                                                                                                                                                                                                    Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T. Ratajczak T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium ions. The activity of this receptor is mediated by a protein that activates a phosphatidylinositol-calcium second
                                                                Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
Thakker R.V.;
                                                                                                                                                     VARIANTS FIH THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
MEDLINE=96311554; PubMed=8733126;
Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L.,
Zimmerman D., Culler G.B. Jr.,
"Mutations in the Ca(2+)-sensing receptor gene cause autosomal
dominant and sporadic hypoparathyroidism.";
Hum. Mol. Genet. 5:601-606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
 human Ca(2+)-sensing receptor gene.";
J. Clin. Endocrinol. Metab. 80:2594-2598(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1;
IsoId=P41180-1; Seguence=Displayed;
                                     AND TYR-582.
                                       VARIANTS NSHPT LEU-227 AND TYR-582
MEDLINE=96292293; PubMed=8675635;
                                                                                                                                                                                                                                                                VARIANT FHH ARG-174, MEDLINE=97442275; PubMed=9298824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT FHH GLU-557
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M MIM, 146200. The Grant of plasma membrane, TAS.

R MO, GO: 00004930; F:G-protein coupled receptor activity, TAS.

R GO; GO: 0000435; F:phosphoinositide phospholipase C activity; TAS.

R GO; GO: 00005813; P:calcium ion homeostasis; TAS.

R GO; GO: 0000513; P:calcium ion sensing; TAS.

R GO; GO: 0000535; P:chemosensory behavior; TAS.

R GO; GO: 0000785; P:chemosensory behavior; TAS.

R GO; GO: 0000785; P:chemosensory behavior; TAS.

R GO; GO: 0000563; P:morphogensis; TAS.

R GO; GO: 0001503; P: 00016001; TAS.

R GO; GO: 0001503; P: 00016001; TAS.

R GO; GO: 0001503; P: 00016001; TAS.

R GO; GO: 0001503; P: 00016001; TAS.

R GO; GO: 0001503; P: 00016001; TAS.

R Ffam; PRO01094; ANF receptor.

R Ffam; PRO01094; ANF receptor; 1.

R FAM; PRO01094; ANF receptor; 1.

R R MINTS; PRO0248; GERMGR.

R ROSITE; PSO0990; G PROTEIN RECEP F3 1; 1.

R ROSITE; PSO0990; G PROTEIN RECEP F3 2; 1.

R ROSITE; PSO0990; G PROTEIN RECEP F3 3; 1.

R ROSITE; PSO0990; G PROTEIN RECEP F3 3; 1.
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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hypoparathyroidism (FIH) [MIM:146200]. FIH is characterized by hypocalcemia and hyperphosphatemia due to inadequate secretion of parathyroid hormone. Symptoma are seizunes, tetany and cramps. SIMILARITY: Belongs to the G-protein coupled receptor family 3.
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EMBL, U20759, AAA86503.1;
EMBL, D50855, BAA09453.1;
EMBL, S83175, AAA864873.1;
EMBL, S68032, AAB35262.2;
EMBL, S68032, AAB35414.1;
EMBL, S68036, AAB29414.1;
EMBL, S81755, AAA14370.1;
EMBL, S81755, AAD14370.1;
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MIM; 601199;
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Best Local Simi
Matches 782;
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Lombardi M., Butters R., Kifor sbert S.C.;

Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor Sun A., Hediger M.A., Lytton J., Hebert S.C., "Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid.", Nature 366:575-580(1993).

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QORSQQQPRCK-QKVIFGSGTVTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRH- 1010
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                                                                                                               413 HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN
                                                                                                                                                                 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILMSG
EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF
            HLRISYNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNS
                                                                                                                                                   MGEQVDFDDQGDLKGNYT11NWQLSAEDESVLFHEVGNYNAYAKPSDRLN1NEKK1LWSG
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01-JUN-1994 (Rel. 29, Last seq
05-JUL-2004 (Rel. 44, Last ann
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                                                                                             -i-FUNCTION: Senses changes in the extracellular concentration of calcium ions. The activity of this receptor is mediated by a G-protein that activates a phosphatidylinositol-calcium second
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R InterPro; IPR00068; Ca_Sens_receptor.
R InterPro; IPR000068; Ca_Sens_receptor.
R InterPro; IPR00003; 74m_3; GPCR_Mgr.
R Pfam; PF00009; 74m_3; J.
R Pfam; PF00009; 74m_3; J.
R PR051TE; PS00949; GPROTEIN RECEP_F3_1; 1.
R PROSITE; PS00980; GPROTEIN RECEP_F3_2; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
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R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
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R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS00980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS009980; GPROTEIN RECEP_F3_3; 1.
R PR051TE; PS009980; GPROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular calcium-sensing receptor.
Extracellular (Potential).
                                                                                                                                                          messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
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7 (Potential).
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Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).

Name=CASR; Synonyms=GPRC2A, PCAR1;

Last sequence update)
Last annotation update)

Chordata, Craniata, Vertebrata, Euteleostomi, Cetartiodactyla, Ruminantia, Pecora, Bovidae,

Bos taurus (Bovine). Eukaryota, Metazoa, C Mammalia, Eutheria, C

NCBI_TaxID=9913;

Bovinae;

SEQUENCE FROM N.A. TISSUE=Parathyroid; MEDLINE=94077182; PubMed=8255296;

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                                               KNEYKAFLRTI PNDEQQATAMAEI I EHFOWNWYGTLAADDDYGRPGIDKFREEAVKRDIC
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STANDARD;

RESULT 4
CASR_RAT
ID _CASR_RAT
AC P48442;
DT 01-FEB-1996 (
DT 01-FEB-1996 (

Db 832 FVSAVEVIAILAASFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHAFKVAARATIRR 891 Qy 900 SAASRKRSSELGGSTISSPASSTGPG	PREDINT 5 OHOURS: OHORD: OHOURS: OHORS:
FT CARBOHYD 130 130 N-linked (GLONAC) (Potential). FT CARBOHYD 261 261 N-linked (GLONAC) (Potential). FT CARBOHYD 287 287 N-linked (GLONAC) (Potential). FT CARBOHYD 468 468 N-linked (GLONAC) (Potential). FT CARBOHYD 468 468 N-linked (GLONAC) (Potential). FT CARBOHYD 541 541 N-linked (GLONAC) (Potential). FT CARBOHYD 541 SM-linked (GLONAC) (Potential). FT CARBOHYD 542 N-linked (GLONAC) (Potential). FT CARBOHYD 543 N-linked (GLONAC) (Potential). FT CARBOHYD 544 N-linked (GLONAC) (Potential). FT CARBOHYD 544 N-linked (GLONAC) (Potential). FT CARBOHYD 73.78; Score 3996; DB 1; Length 1079; Best Local Similarity 73.78; Pred. No. 6.5e-272; Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps	1 MACHICALFLOGTHLOGHNOCAPHORADOWNOLDHIGGE PHIRICALPHICALANDODLISTB 6 1 MASYSCCLALLALAMISSANGEOCAPACKED ILICALFPHIRICAL

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             THLRISYNVYVAVYSIAHALODIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTN
IDESEMISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIMLAS
                                                                             NCYFTEKTLIQLK-NSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDY
                                                                                                                                                         SMGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWS
                                      EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETF
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CASR MOUSE STANDARD; PRT; 1079 AA.
090Y96; 008968; 088519; 090Y95; 090ZU8; 09R1D6; 09R1Y2;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Call calcium-sensing receptor).
Name=Casr; Synonyms=Gprc2a;
                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Epiphyseal cartilage;
MEDLINE=20043955; PubMed=10579354;
Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A.,
Miller S., Shoback D.;
"Expression and signal transduction of calcium-sensing receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOUGHING OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.
SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.
OUATION THATLE J.E. II. Siddhanti S.R., Guo R., Hinson T.K.,
"A distinct cation sensing mechanism in MC3T3-E1 osteoblasts
functionally related to the calcium receptor.",
J. Bone Miner. Res. 12:393-402(1997).
-!-FINCTION: Senses changes in the extracellular concentration of
calcium ions. The activity of this receptor is mediated by a G-
protein that activates a phosphatidylinositol-calcium second
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                                                                                                         "The calcium sensing receptor and its alternatively spliced form murine epidermal differentiation.";
J. Biol. Chem. 275:1183-1190(2000).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
STRAIN=Black Swiss X 129/SVJ; TISSUE=Kidney;
MEDLINE=20119279; PubMed=10652312;
Pi M., Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;
"Sensing of extracellular cations in CasR-deficient osteoblasts.
Bvidence for a novel cation-sensing mechanism.";
J. Blol. Chem. 275:3256-3263(2000).
                                                        Mauro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NWRI; TISSUE=Brain;
Hildenbrand J., Ammon H.P.T., Wahl M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
Moawad T.I., Riccardi D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                       MEDLINE-20092890; PubMed=10625662;
Oda Y., Tu C.-L., Chang W., Crumrine D., Koemueves L.,
Elias P.M., Bikle D.D.;
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SUBCELLOUAR LOCATION: Integral membrane protein.
ALTERNATUS PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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HSSP; PC3385; LEWK.
MGI:1351351; Gprc2a.
InterPro; IPR001828; ANF_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage and bone.";
Endocrinology 140:5883-5893(1999).
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EMBL, AFILO179, AAD28372.1; --
EMBL, AF128842; AAC1638.1; --
EMBL, AF068900; AAC19388.1; --
EMBL, AR027140; BAA77688.1; --
EMBL, AF0020115; AAC3352.1; --
EMBL, AF159565; AAF00193.1; --
STRAIN=C57BL/6; TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=B;
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   DAR DER BERTARE BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER BERTER
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485

553 545 613 605 673 665 733 725 793 785 853 845 913 905 936 964

us-10-016-496-2.rup

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SIAHALQDIHSCKPGTGIFANGSCADIKKVBAWQVLNHLLHLKFTNSMGEQVDFDDQGDL 493
                 QLEFIADVIONSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIMLASEAWASSSLIAKPEY
                                                                                                                                                                                                                               VGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEGKILWSGFSREVPFSNCSRD
                                  251 BIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKEIVRRNITGRIMLASEAWASSSLIAMPEY
                                                                 FHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETFNCYFTEKTLTQLK-
                                                                                                                  NSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYTHLRISYNVYVAVY
                                                                                                                                SIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDL
                                                                                                                                                                                                                 KGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPFSNCSRD
                                                                                                                                                                                                                                                                 CVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSNENHTSCIAKEIEY
                                                                                                                                                                                                                                                                                CQAGTRKGIIBGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSNENYTSCIAKEIBF
                                                                                                                                                                                                                                                                                                                  LSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSYLLLFSLICCFSSS
                                                                                                                                                                                                                                                                                                                                 LLVFLCTFMQIVICIIMLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTCLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LTMEMQ-----RCST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906 TGSNPSSSISSKSNSEDRFPQPERQKQQQPLALTQQEQQQQPLTLQPQQQQQPQQPRCK-
                                                                                                                                                                                                                                                                                                                                                                 LIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSLHRKWVGLNLQF
                                                                                                                                                                                                                                                                                                                                                                                         666 LFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSFHRKWWGLNLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKFVSAVEVIAILASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRSAASRKRSSSLCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  937 QKVSFGSGTVTLSLSFEETGRYATLSRTARSRNSADGRSGDDLPSRHHDQGPPQKCEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                  LLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMALGFLIGYTCLLAA
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SEQUENCE FROM N.A.
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                                                                                                                 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNKNEYKAFLRTIPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPEATKCIRYNFRGFRW
                                                                                                                                                  Extracellular calcium-sensing receptor.
Extracellular (Potential).
1 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
InterPro; IPR000068; Ca sens_receptor.
InterPro; IRR000337; GPCR_MGF.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMS.
PRINTS; PR00248; GPCRMS.
PROSITE; P800960; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; P800981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; P800981; GPROTEIN_RECEP_F3_3; 1.
PROSITE; P800981; GPROTEIN_RECEP_F3_3; 1.
ALLETHATIVE SP1259; G PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3976.5; DB 1; Length 1079;
Pred. No. 1.5e-270;
3; Mismatches 124; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                                              Fundamental (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).

N-linked (GlCNAc...) (Potential).
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                                                                                                                                                                                                                                      Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                            (Vtoplasmic (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
3 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 and 3).
                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
                                                                                                                                       Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.5%;
74.3%;
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                                                                                                                                       1079
612
612
635
649
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1057
1064
1076
                                                                                                                           Signal; Transmembrane
SIGNAL
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610
814
889
906
1057
1064
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CARBOHYD
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CARBOHYD
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OGAME;
OS-JUL-2004 (TrEMBLrel. 27, Created)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Salmo salar (Atlantic salmon).
Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei;
Protacanthopterygii; Salmoniformes; Salmo.

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LIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETFNCYFTEK 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nearing J.A., Harris W.;
"Tissues of Atlantic Salmon (Salmo salar) Express Multiple Polyvalent
Cation Sensing Receptor (CaR) cDNAs that Appear to Mediate Salinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPEATKCIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |- |||: : : | |||:||||| |||:|||||| LVLLGFSSV----ISTYGPHQRAKTGDILLGGLFPMHFGVTSKDQDLAARPESTECVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLIQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYTHLRISYN
                                                              AILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRSAASRKRS
                                     TCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKFVSAVEVI
GLNLQFLLVFLFTFVQVMICVVWLYNAPPASYRNHDI-DEIIFITCNEGSMMALGFLIGY
                                                                                                                                                                                                                                                                                                                             AAP79925
AAP79925,
AAP79925,
03-MAR-2004 (TrEMBLrel. 27, Created)
03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Calcium polyvalent cation receptor 1.
Salmo salar (Alantic salmon).
Actinopterygii, Neopterygii, Teleostei; Euteleostemi,
Protacanthopterygii, Salmoniformes; Salmonidae; Salmo.
11.1 TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                 SSVGGSCASTPSSSISLKTNDNDSPSGQQRIHKPRVSFGSGTVTLSLSFEES
                                                                                                                                                                                             SSLCGSTISSPASS ----TCGPGLTMEMQRCSTQKVSFGSGTVTLSLSFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AY245445; AAP79925.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        941 AA; 106130 MW; 06119219CDF62D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.9%; Score 3728; DB 2; 74.7%; Pred. No. 3.9e-253; ive 97; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 74.7%;
Matches 711; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
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              Nearing J.A., Harris W.;

Nearing J.A., Harris W.;

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0004872; Freegetor activity; IEA.

InterPro; IPR001828; ANF receptor.

R InterPro; IPR001828; ANF receptor.

R InterPro; IPR00137; GZER Mgr.

R InterPro; IPR001500; NCD3G_GPCR.

R Pfam; PF001094; ANF receptor; 1.

R Pfam; PF001094; ANF receptor; 1.

R Pfam; PF001094; ANF receptor; 1.

R Pfam; PF001094; GZERNGR.

R PRINTS; PR00529; GZERNGR.

R PRINTS; PR00248; GZERNGR.

R PROSITE; PS00979; GZERNGR.
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                                                                                                                                            124 NLDEFCNCTDHIPSTIAVVGASGSAVSTAVANLLGLFYIPQISYASSSRLLSNKNQFKSF 183
                                                                                                                                                                               LLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPBATKCIRY
                                NFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALBATLSFVAQNKIDSL
                                                                                                                             NLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNKNEYKAF
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                                                                                                                                                                                                                                                                                                                                                                                                          VYVAVYSIAHALQDIHSCKPGTG1FANGSCAD1KKVEAWQVLNHLLHLKFTNSMGEQVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPF
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CCFSSSLIFIGEPODWTCRLROPAFGISFVLCISCILVKTNRVLLVFEAKIPTSLHRKWW
                                                                                                                 525 SNCSEDCEPGTRKGIIESMPTCCPECTECSEGEYSDHKDASVCTKCPNDSWSNBNHTSCP
                                                                                                                                                                       585 LKEIEFLSWTEPFGIALALCSVLGVFLTAFVMGVFIKFRNTPIVKATWRELSYLLLFSLI
                                                                                                                                                                                                                                                                    GLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMALGFLIGY
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                                                                                                                                                                                                                                                                                                                                                                                              824 AILASSFGLLACIFFKVYIILFKPSRNTIEEVRCSTAAHSFKVAAKATLRHSSASRKRS
                                            DDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPF
                                                            SNCSRDCVPGTRKGI I EGEPTCCFECMACAEGEFSDENDASACTKCPNDFWSNENHTSCI
                                                                                                                                                      608 AKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSYLLLFSLI
                                                                                                                                                                                                                                                                                                                                                    764 TCLLAAICFFFAFKSRKLPENFTEAKFITFSMLIFFIVWISFIPAYFSTYGKFVSAVEVI
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Calcium polyvalent cation receptor 2.
Salmo salar (Atlantic salmon). Protaco, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neoperygii, Teleostei; Euteleostei, Protaconthopterygii, Salmoniformes, Salmoniae, Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SSLCGSTISSPASS----TCGPGLTMEMORCSTQKVSFGSGTVTLSLSFEET 955
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TISSUB-Kidney,

Nearing U.A., Harris W.;

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

By Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR000328; ANF receptor.

R InterPro; IPR000328; ANF receptor.

R InterPro; IPR00038; CG_Sens receptor.

R InterPro; IPR011500; NCD3G_GPCR.

R Ffam; PR00003; 7tm 3; 1.

R Pfam; PR07562; CASBNSINGR.

R PRINTS; PR00529; CASBNSINGR.

R PRINTS; PR00248; GPRNGR.

R PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941 AA
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64 NFRGFRWLQAMIFAIDEINNSSTLLPNITLGYRIFDTCNTVSKALBATLSFVAQNKIDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 NLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNKNEYKAF
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                                                                             TCLLAAICFFFAFKSRKLPENFTEAKFITFSMLIFFIWHISFIPAYFSTYGKFVSAVEVI
                                                                                                                                AILASSFGLLGCIYFNKCYIILFKPCRNTIEEVRCSTAAHAFKVAARATLRRSAASRKRS
                                                TCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYVSTYGKFVSAVEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDMed=11932208; MEDLINE=21930045; PubMed=11932208; MEDLINE=21930045; PubMed=11932208; MIS., Bendell L., Power D.M., Warner S., Elgar G., Ingleton P.M.; "Calcitonin: Characterisation and expression in a Teleost fish: Fugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Extracellular calcium sensing receptor.
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llarity 73.2%; Pred. No. 1.5e-251;
Conservative 105; Mismatches 118;
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EMBL, AJ289717; CAC41352.1; -.
HSSP; P23385; IEWK.

GO: 00010016020; C:membrane; IEA.

GO: GO:0008067; F:metabotropic glutamate,

GO: GO:0008067; F:metabotropic glutamate,
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PRINTS; PRO0248; GPCPMGR.
PROSITE; PS00979; G PROTEIN RECEP F3 1; 1.
PROSITE; PS0259; G PROTEIN RECEP F3 1; 1.
                                                                                                                                                                                                                                                                                                                                                               940
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InterPro; IPR000068; Ca Sens receptor.
InterPro; IPR000337; GPCR Mgr.
InterPro; IPR011500; NCD3G GPCR.
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Pfam; PF01094; ANF receptor; 1.
Pfam; PF07562; NCD3G; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 SQYFEEWQIQGLVGRIENSSAKVIVVFASGPDIEPLIKEMVRRNITDRIMLASEAWATTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --QRLRDSE-------NGS-----TSFRPLCTGEEDIMGAETPYLDYTHLRISYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 VYVAVHSIAQALQDILITCIPGRGLFSNNSCADIKKIEAWQVLKQLRHLNFSNSMGEKVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKEIEFLSWTEPFGIALALCSVLGVFLTAFVMGVFIKFRNTPIVKATNRELSYLLLFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLFLGFTLLQSYNVSGYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPEATKCIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFRGFRWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRTIPNDEQQATAMAEIIEHFQWNWVGTLAADDDYGRPGIDKFREEAVKRDICIDFSEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLASEAWASSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 TLTQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGBENITSVETPYLDYTHLRISYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNSMGEQVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENADPSGNYTIINWHRSPEDGSVVFEEVGFYNMRAKRGVQLFIDNTKILWNGYNTEVPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCFSSSLIFIGEPROWTCRLROPAFGISFVLCISCILVKTNRVLLVFBAKIPTSLHRKWV
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Salinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Calcium polyvalent cation receptor 2.
Salmo salar (Atlantic salmon).
Briaryorei, Metasca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                 Nearing J.A., Harris W.;
"Tissues of Atlantic Salmon (Salmo salar) Express Multiple Cation Sensing Receptor (CaR) cDNAs that Appear to Mediate
                                                                                                                                                                                                                                                                                                                                                                                                      68.8%; Score 3721; DB 2; Length 974.6%; Pred. No. 1.2e-252; ive 97; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                          Sensing.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   941 AA; 106072 MW; C72B91C0029DFF27 CRC64;
                                                                                                                                                                                                                                                                                                                           EMBL; AY245443; AAP79923.1;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 74.6%
Matches 710; Conservative
                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Kidney;
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127 123 187

67 63

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QVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSK 543
                                                         .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                               IDSLNLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDSLNLDEFCNCTDHIPATIAVVGAAGSAVSTAVANLLSLFYIPQISYASSSRLLSNKWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 TFCFLKEIEFLAWSEPFGIALAICAVLGVLLTAFVMGVFVRFRNTPIVKASNRELSYVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 FSLICCFSSSLIFIGEPRDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSLH
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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                             35;
                                                         GABA-B-like recepto.
                                                                                                                                                                                                                                                                                 67.4%; Score 3644.5; DB 2; Length 940; 71.6%; Pred. No. 2.9e-247; ive 114; Mismatches 124; Indels 35;
                                                                                                                                                                                                                                                       940 AA; 105813 MW; 06DAB7803B6878B3 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998)
EMBL; AB008857; BAA26122.1; -.
HSSP; P23385; 1EWT.
                                                                                                                                                                                                                                                                                                             Conservative 114; Mismatches
                                                                                                                                                                                  PRINTS; PRO0592; CASENSINGR.
PRO10248; GPCRMGR.
PRO51TE; PS00979; G PROTEIN RECEP F3 1; 1.
PROSITE; PS0259; G PROTEIN RECEP F3 4; 1.
                                         GO; GO:0016020, C:membrane; IEA.
GO; GO:0008605, F:metabouropic glutamate,
GO; GO:0004872; F:metabouropic glutamate,
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000088; Ca Sens receptor.
InterPro; IPR000036; GPGR MgF.
InterPro; IPR011500; NCD3G_GPCR.
                                                                                                                                                        receptor; 1.
                                                                                                                                        Pfam; PF00003; 7tm 3; 1.
Pfam; PF01094; ANF_recept
Pfam; PF07562; NCD3G; 1.
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                           687;
                                                                                                                                                                                                                                             Receptor.
SEQUENCE
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Best Local S
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                                                                                                                                                                          VYVAVYSIAQALQDILTCTPGQGLFANNSCADIKKMBAWQVLKQLRHINYTNSMGBKMHF
                                                                                                                                                                                                                                                                                                                                               CCFSSSLIFIGQPQDWMCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSLHRKWW
                                                           LIAKPEYFHVVGGTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKEFWEETFNCYFTEK
                                                                                                                  VYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVLNHLLHLKFTNSMGEQVDF
  SOYYTOKOLEFIADVIONSSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLASEAWASSS
                                                                                                                                                        368 TLIQLKNSKVPSHGPAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYTHLRISYN
                                                                                                                                                                                                                                                                        DDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWSGFSKVVPF
                                                                                                                                                                                                                                                                                                 465 DENADLAANYTLINWHRSAEDGSVVFEEVGYYNMHAKRGGKLFIDNTKILWNGFSSEVPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 TCLLAAICFFFAFKSRKLPENFTEAKFITFSMLIFFIVWISFIPAYFSTYGKFVSAVEAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Putative pheromone receptors related to the Ca2+-sensing receptor Fugu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-982126788; PubMed=9560249;
Naito T., Saito Y., Yanamoto J., Nozaki Y., Tomura K., Hazama M., Nakanishi S., Brenner S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2003 (TrEMBLrel. 24, Last annotation update)
Calcium2+ sensing receptor.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
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Nearing J.A., Harris W.;
"Tissues of Atlantic Salmon (Salmo salar) Express Multiple Polyvalent
Cation Sensing Receptor (CaR) cDNAs that Appear to Mediate Salinity
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03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Calcium polyvalent cation receptor 3.
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bu
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmo.
NCBI_TaxID=8030;
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Submitted (FEB-2003) to
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AAP79924;
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Calcium polyvalent carion receptor 3.
Calcium polyvalent carion receptor 3.
Salmo salar (Atlantic salmon).
Cabraryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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llarity 75.5%; Pred. No. 4.6e-234;
Conservative 88; Mismatches 99;
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STRAIN=C57BL/6J; TISSUE=Testis;
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930542118 product:calcium-sensing receptor, full
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50.0%; Score 2707.5; DB 2; Length
Best Local Similarity 70.8%; Pred. No. 1.9e-181;
Matches 533; Conservative 56; Mismatches 109; Indels
PRINTS; PR00592; CASENSINGR.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00990; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
Receptor.
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SEQÜENCE 783 AA; 87795 MW; 64BAE914566E19D5 CRC64;
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